#### SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: GAMBEL Examiner #: 70675 Date: Higlot
Art Unit: Phone Number 30 Serial Number:
Mail Box and Bldg/Room Location: Results Format Preferred (circle). PAPER DISK E-MAIL
If more than one search is submitted, please prioritize searches in order of need.
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.
Title of Invention: 08/487283.
Inventors (please provide full names):
Earliest Priority Filing Date:
*For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the
appropriate serial number.
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() SQ 10 NO: 8 AA
2) Ser 10 NO: & NA
(3) seq 10 NO: [VAS
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9 SQID NO: 12 (1-124AA)
(5) 8-12 OF SER 10 NO:1 CLOSED
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1/41/41/W2065X 030
STAFF USE ONLY Type of Search Vendors and cost where applicable
Searcher: NA Sequence (#) STN
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Searcher Location: Structure (#) Questel/Orbit
Date Searcher Picked Up: 3 19 Bibliographic Dr.Link
Date Completed: Lexis/Nexis
Searcher Prep & Review Time: Fulltext Sequence Systems
Clerical Prep Time: Patent Family WWW/Internet
Online Time: Other Other (specify)

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P82263 PRELIMINARY; PRT; 20 AA. P82263; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) ALLERGEN ASP F 3 (FRAGMENT). Aspergillus fumigatus (Sartorya fumigata).
                                                                                                                                                                                                                                                                                                     Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.; "A calcyclin-associated protein is a newly identified member o cat/phospholipid-binding proteins, annexin family."; J. Biol. Chem. 267:8919-8924(1992).

HSSP; P13214; IANN.

SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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SSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
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Pred. No. 3.9e+02;
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B8272D8940BD0B41 CRC64;

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01-WAY-2000 (TFEMBLEEL 13, Last annotation update)
40.5 KDA IGA NEPHROPATHY-ASSOCIATED OUTER MEMBRANE ANTIGEN (FRAGMENT).
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Eukaryota; Fungl; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
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SEQUENCE 20 AA, 2153 MW, 4CD523E74E5639E5 CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
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"80 kDa mouse sperm protein as a substrate of protein kinase C.";
Chem. Phaem. Bull. 40:2780-2782(1992).
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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                                                                                                               Sarma P.U., Gupta T.M., Fairwell T.;
Submitted (DEC-1999) to the SWISS-PROT data bank.
-!- FUNCTION: BINDS TO IGG AND IGE.
Allergen; IgE-binding protein; IgG-binding protein.
                                                                                                                                                                                                                                                                                               Score 29; DB 3; L Fred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                 27.1%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
MEDLINE=96215401; PubMed=8625525;
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MEDLINE=93099617; Pubmed=1464108;
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                 STRAIN-AF-285;
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Q9R4D2;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                   Gaps
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STRAIN=SP1 FROM REUNION ISLAND;
MEDLINE=97049057; PubMed=8893787;
Peterschmitt M., Granier M., Frutos R., Reynaud B.;
"Infectivity and complete nucleotide sequence of the genome of genetically distinct strain of maize streak virus from Reunion
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STRAIN=SP1 FROM REUNION ISLAND;
Isnard M., Granler M., Frutos R., Reynaud B., Peterschmitt M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marty I., Brugidou C., Chartier Y., Meyer Y.; "Growth-related gene expression in Nicotiana tabacum mesophyll
  Length 17;
                                                   4; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update).
17.6 KDA REPB PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ELONGATION FACTOR 1-A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize streak virus.
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=10821;
Score 25; DB 11;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 10;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                            18 AA
                                                2; Mismatches
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MEDLINE=94035181; PubMed=8220482;
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23.4%;
50.0%;
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18 AA; 1983 MW;
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35.78;
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EMBL; Z14080; CAA78458.1;
                                                   6; Conservative
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DPTGAKVTKAAQKK 16
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Matches 4
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O93047;
O93047;
O1-NOV-1998 (TrEMBLrel. 0
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ224999; CAA12284.1; -.
NON_TER 21 21
SEQUENCE 21 AA.
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093046;
01-NOV-1998
01-NOV-1998
                                                                                       Maize streak virus.
Viruses; ssDNA viru
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NON_TER 21 21
   SEQUENCE FROM N.A.
                                                         NCBI_TaxID=10821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SP1 FROM REUNION ISLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Infectivity and complete nucleotide genetically distinct strain of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97049057; PubMed=8893787; Peterschmitt M., Granier M., Frutos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssDNA viruses; NCBI_TaxID=10821;
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3 (TrEMBLrel.
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                                                                                       viruses;
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44

    08, Created)
    08, Last sequence up
    08, Last annotation
    (FRAGMENT).

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                                                                                       Geminiviridae;
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Pred.
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No.
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streak virus
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                                                                                          Mastrevirus
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Q75729;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ2
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SEQUENCE
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                 Rattus norvegicus (Rat)
                                                          R-RAS GAP
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000583; -
PROSITE; PS00443; GATA:
SEQUENCE 12 AA; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mariani R., Kirchhoff F., Greenough Desrosiers R.C., Skowronski J.; Submitted (JUN-1996) to the EMBL/Gen EMBL; U61801; AAB04720.1;
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                                                                          R-RAS GTPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-HP94F1
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1238 MW; 2B921E1187B325A3
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Chordata;
Rodentia;
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71.4%;
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PROTEIN (FRAGMENT).
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Pred. No. 2e+C
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Craniata; Vert
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Euteleostomi;
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MEDLINE=92202192; PubMed=1313009;
                                           Arch. Virol. 141:1637-1650(1996)
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Best Local Similarity 37.5
Matches 6; Conservative
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Mizuteni A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
Kobayashi R., Hidaka H.;
"CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblast 371 cells.",
J. Biol. Chem. 267:13498-13504(1992),
SEQUENCE 19 A3, 2144 MW; F3994AFDODE7CB05 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.

NCBI_TaxID=9913;
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STRAIR-SP2 FROM REUNION ISLAND;
MEDLINE-97049057; PubMed-8893787;
Peterschmitt M., Granter M., Frutos R., Reynaud B.;
"Infectivity and complete nucleotide sequence of the genome of geneticably distinct strain of maize streak virus from Reunion
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CALCYCLIN-ASSOCIATED PROTEIN PEPTIDE L-11, CAP-50-ANNEXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 11; Length 18;
Pred. No. 2.6e+03;
6; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                           Iwashita S., Kobayashi M.;
"NGF-mediated downregulation of R-ras GAP expression.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB020479; BAA7868.1; -...
                                                                                                                                                                                                                                                                                                                                              6BC3355FDC91E28A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maize streak virus.
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=10821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 6; 1
Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TEMBLRE). 08, Last: 01-NOV-1998 (TEMBLRE). 08, Last: 17.6 KDA REPB PROTEIN (FRAGMENT). REPB.
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41.7%;
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                                                                                                                                                                                                                                                                                                                                              18 AA; 2104 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 41.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VEEEGLRVFQSVRIKI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IDHQGTKSSKCVRQKV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                       SEQUENCE FROM N.A.
STRAIN-SPRAQUE-DAWLEY;
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NCBI_TaxID=10116;
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SEQUENCE
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093050
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DT 01-NOV
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Q9TRQ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T., Iwanaga S., Hirata M.;
Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
SEQUENCE FROM N.A.
STRAIN=SP2 FROM REUNION ISLAND;
Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
"Quasispecies nature of three related maize streak virus isolates obtained through different mode of selection.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ225005; CAA12297.1; -.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                          22.4%; Score 24; DB 14; Length 21; 44.4%; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosol.";
J. Biol. Chem. 267:6518-6525(1992).
SEQUENCE 13 AA; 1537 MW; 3EA2F724AD8B85B8 CRC64;
                                                                                                                                                                                                                                                                       SEQUENCE 21 AA; 2378 MW; 267B619FB848A32B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Pred. No. 2.3e+03;
2; Mismatches 5;
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Best Local
                                                                                                                       Matches
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Best Local :
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Q9LMD7;
Q9LMD7;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
[1]
                                                                                                                                                                                                                                                                     Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC068602; AAF79279.1; -. SEQUENCE 17 AA; 1987 MW; 518CAC484C814DE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Conn L., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
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EMBL; AF067195; AAC79991.1; -.
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Local Similarity 35.7%;
nes 5; Conservation
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HHLSPSSRC
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4; Conserv
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16
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                                                                                                                 : Score 23; DB
: Pred. No. 3.6e
2; Mismatches
                                                                                                                                                                                                                                                                  518CAC484C814DE6 CRC64;
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Pred. No. 3.2e+03;
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                                                                                                                                                    3.6e+03;
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107
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AAW85479
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                                                                                  Pro-C5 polypeptide
Synthetic fibring
EVII/TE multi-prot
Factor-VII-derived
Factor VII peptide
EVII/TE multi-prot
Factor-VII-derived
Mouse GP88 autocri
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Telomerase peptide
HIV p17 gag protei
HIV p17 gag protei
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Cytotoxic T lympho Beta-casein fragme HIV pl7 gag protei HIV pl7 gag p	ag I ag I dyl dyl dyl dyl dyl i nke ocal

## ALIGNMENTS

AAR77605 ID AAR7 XX

AAR77605 standard; Protein;

21 AA

RESULT

Evans MJ, Matis L, Mueller EE, Nye SH, Rother RP, Springhorn J P, Squinto SP, Wang Y, Wilkins JA; Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; KSSKC epitope. Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis WPI; 1995-392923/50. 01-MAY-1995; 09-NOV-1995. Homo sapiens. Pro-C5 polypeptide KSSKC epitope 02-APR-1996 AAR77605; 02-MAY-1994; W09529697-A1 (ALEX-) ALEXION PHARM INC. (first entry) 94US-0236208 95WO-US05688 Rollins S; Thomas TC;

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Synthetic.
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                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibrinogen; C-terminus; cell adhesion; cell binding; proliferation; wound healing; diabetes mellitus; clotting; coagulation; disorder; haemophilla A; factor VIII deficiency; haemophilia B; factor IX deficiency; cell culture; separation; cell transplantation;
                                                             The cDNA sequence of the complement C5 gene transcript predicts a secreted pro-C5 precursor of 1676 amino acids (AAR77604). C5 is a beta-globulin heterodimer thought to play a role in the pathogenesis of glomerulonephritis (GN). Cleavage of the C5 alpha-chain by a convertase enzyme generates anaphylatoxic C5a. Monoclonal and humanised recombinant antibodies that recognise the alpha-chain KSSKC epitope (AAR77605) block C5a generation, thereby reducing glomerular inflammation and kidney dysfunction associated with GN.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides corresponding to fibrinogen carboxy terminus, used for
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                      Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic fibrinogen C-terminus peptide, peptide-07.
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 107; DB 16;
100.0%; Pred. No. 4.6e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic structure; research tool; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HADA-) HADASIT MEDICAL RES SERVICES & DEV. (VITE-) VI TECHNOLOGIES INC.
                  Example 13; Page 81; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 12; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
---nhas 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoting wound healing
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                                                                                                                                                                                                                                                                                              21 AA;
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                                                                                                                                                                                                                                                                                              Sequence
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cellular product, e.g., diabetes mellitus type I, haemophilia A (factor VIII deficiency), and haemophilia B (factor IX deficiency). They can also be used for the growth and transport of cells in cell culturing systems, the separation of different types of cells from mixed cell cultures, and the transplantation of cells into tissues or cell cultures, and the transplantation of cells into tissues or cell cultures, prosthetic devices or collagen sheets. The peptides can also be used as tools for performing analysis of other physiological systems, and for further research and development, for example, to identify and isolate cell receptors. The peptides can also be used in diagnosis, e.g., of blood coagulation disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic peptides (AAR67858-R67865) were individually assayed as test substances to ascertain their effect on the formation of the bloodclotting factor VII/tissue factor multi-protein complex. Of the peptides tested, the most inhibition was obtained with cyclic peptides representing the ring structures present in the FVII growth factor domains (i.e. AAR67861, AAR67864). Peptide AAR67865, a linear peptide corresp. to residues 136-146 from a region close to the site of cleavage which activates FVII also had good inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Factor VII; Factor 7; blood clotting factor; multi-protein complex; human tissue factor; FVII/TF; assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          due
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 21; Length 19;
Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR67862 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-GB01314.
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Matches 6; Conserv
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RESULT

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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                         Matches
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                          This peptide fragment is useful for preparing pharmaceutical compositions for prevention or inhibition of Factor-VII binding to tissue factor. It is useful for treating or preventing blood clotting disorders in humans and animals, e.g. thrombosis, angina, cerebrovascular disease or pulmonary embolism.
        Factor VII peptide analogue
                            06-SEP-1990 (first entry)
                                                                                                                                                                                                                                                                                                         Factor VII-derived peptide compounds - useful for preventing/inhibiting binding of tissue factor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR68909;
                                                AAR05852
                                                                   AAR05852 standard; protein; 11 AA
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                       WPI; 1995-052003/07.
                                                                                                                                                                                                                                                                                                                                                           Orning L,
                                                                                                                                                                                                                                                                                                                                                                             (HAFS-) HAFSLUND NYCOMED AS (HOLM/) HOLMES M J.
                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-1993;
10-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerebrovascular disease; pulmonary embolism; heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Factor-VII; blood-clotting factor; thrombosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Factor-VII-derived peptide
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|| ||| |
2 dhtgtkrs 9
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                                                                                                                 DHQGTKSS 10
                                                                                                                                                         Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                          Sakariassen
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                      Page 20; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          93GB-0012601.
94GB-0009335.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                   29.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                          KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment FVII-4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                         0;
                                                                                                                                                         Score 32; DB Pred. No. 3.4e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Stephens RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 16;
Pred. No. 3.4e+05;
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                                                                                                                                                                  DB 16;
3.4e+05;
                                                                                                                                                                                                                                                                                                                                                          Sakariassen
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                                                                                                                                                                             Length 9;
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Matches
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Immunoassay for multi-protein complexes - used to detect malfunction in formation of complexes in an individual, to genetic or physiological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One or both of the two C-terminal residues may be absent, the peptide is useful in inhibiting formation of active tissue factor VII complex and thus blood clotting.
                                           WPI; 1995-052226/07
                                                                                                                                                          05-JAN-1995
                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                       Factor VII; Factor 7; blood clotting factor; multi-protein complex;
human tissue factor; FVII/TF; assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New clotting factor VII peptide analogues - useful for inhibiting blood clotting induced by tissue factor
                                                              Oerning L,
                                                                                 (HAFS-) HAFSLUND NYCOMED AS (HOLM/) HOLMES M J.
                                                                                                                18-JUN-1993;
                                                                                                                                      17-JUN-1994;
                                                                                                                                                                              WO9500847-A
                                                                                                                                                                                                                                                     FVII/TF multi-protein complex inhibition test peptide FVII-4
                                                                                                                                                                                                                                                                        07-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                               AAR67860;
                                                                                                                                                                                                                                                                                                                   AAR67860 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pepe MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor VII; blood clotting; Tissue factor; TF; thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9003390-A.
                                                                                                                                                                                                                                                                                                                                                                                                            y Match 29.9%;
Local Similarity 75.0%;
hes 6; Conservative
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| 3 dhtgtkrs 10
                                                                                                                                                                                                                                                                                                                                                                                         3 DHQGTKSS 10
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                                                             Sakariassen K,
                                                                                                                 93GB-0012638
                                                                                                                                      94WO-GB01314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB Pred. No. 57; 0; Mismatches
                                                              Stephens
                                                              77
                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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           e.g.
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canulin; epithilin; mouse; growth factor; autocrine; tumou
viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                                                                                                                                                                                                                     Mouse GP88 autocrine growth factor antigenic peptide S14R.
                                                                                                                                                                 AAW85479 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-045276/04.
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3 rgtkclrkki 12
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                                            || || |
dhtgtkrs 9
                       DHQGTKSS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AA;
                                                                                                                                                                                                                                                                                                                             GP88; granulin;
                                                                                                                                                                                                                                             15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9852607-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serrero G;
                                                                                                                                                                                                         AAW85479;
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Best Local S
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                                                                                                                          RESULT
AAW85479
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                                                                                                                                                                                                         NAME OF COLOR OF STATE OF STAT
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                                                      Synthetic peptides (AAR67858-R67865) were individually assayed as test substances to ascertain their effect on the formation of the bloodclotting factor VII/tissue factor multi-protein complex. Of the peptides tested, the most inhibition was obtained with cyclic peptides representing the ring structures present in the FVII growth factor domains (i.e. AAR67861, AAR67861, and AAR67863). Peptide AAR67863, a linear peptide corresp. to residues 136-146 from a region close to the site of cleavage which activates FVII also had good inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This peptide fragment is useful for preparing pharmaceutical compositions for prevention or inhibition of Factor-VII binding to tissue factor. It is useful for treating or preventing blood clotting disorders in humans and animals, e.g. thrombosis, angina, cerebrovascular disease or pulmonary embolism.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Factor VII-derived peptide compounds - useful for preventing/inhibiting binding of tissue factor to factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Factor-VII; blood-clotting factor; thrombosis; angina; cerebrovascular disease; pulmonary embolism; heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 16; Length 11;
Pred. No. 57;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                           Length 11;
                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakariassen K;
                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor-VII-derived peptide fragment FVII-4
                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephens RW,
                                                                                                                                                                                                                                                                                                                             Score 32;
                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 20; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR68908 standard; peptide; 11 AA
                     Page 8; 19pp; English.
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Best Local Similarity 75.0%;
Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                           29.9%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-052003/07.
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                                                                                                                                                                                                                                                                  11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         3 DHQGTKSS 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-1994;
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                  Example 2;
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                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                 Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   And residues 8562-R875 of murine GP88 (see AAM85474). GP88 is an acid residues 8562-R875 of murine GP88 (see AAM85474). GP88 is an acid residues 8562-R875 of murine GP88 (see AAM85474). GP88 is an atightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. S14R was used to raise neutralising antibodies to GP88 is such as anti-GP88 antibodies used to treat diseases associated with increased expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to GP88-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of peptide S14R, comprising amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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5; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 45; 86pp; English.
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40.0%;
                                                           97US-0991862.
97US-0863079.
98WO-US10555
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       especially, breast, lung, ovarian, cervical, colorectal, prostate or pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary tract carcinomas. They are useful for generating telomerase T lymphocytes capable of recognising and destroying tumour cells in a mammal, comprising culturing T lymphocytes obtained from the mammal with the peptides. Telomerase protein is expressed only by tumour cells, hence, other body cells are not targeted or destroyed by telomerase specific T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a telomerase peptide of the invention, be used in a method for the treatment or prophylaxis of cancer sequences are useful in the treatment or prophylaxis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaudernack G, E
Saeboe-Larsen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma; telomerase T lymphocyte.
            Human immunodeficiency virus type
                                                 HIV: human immunodeficiency virus; antigen; conjugated peptide; pl7 gag protein; T_cell specific binding peptide; TH1; TH2; AIDS;
                                                                                                                                                                    AAW55855 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein or peptide fragments useful in cancer in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telomerase peptide #174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-2000 (first entry)
                                                                                       HIV p17 gag protein antigenic peptide HIV-1HAN.
                                                                                                                   21-JUL-1998
                                                                                                                                             AAW55855;
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                  major country equivalent to NO9803141.
                                                                                                                                                                                                                                                                                                                                                                                                 Note: This sequence was indexed from WO200002581, which is the first
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                                       lmmune response;
                                                                                                                                                                                                                                                                 12 CVRQKVEGS 20
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                                                                                                                                                                                                                                                                                                                                                           9 AA;
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                  (first entry)
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                                       HGP-30
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                                                                                                                                                                                                                                                                                                       . 68;
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                                                                                                                                                                                                                                                                                        Score 31; DB 21;
Pred. No. 3.4e+05;
2; Mismatches 2
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RESULT 11
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ID AAW558
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an HIV pl7 gag protein antigenic peptide species specific sequence from the present invention. The present invention describes a conjugated peptide which is capable of eliciting a TH1 response when administered to a human. The
                                                                                                                                                                                HIV; human immunodeficiency virus; antigen; conjugated peptide; pl7 gag protein; T_cell specific binding peptide; TH1; TH2; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New conjugated peptide(s) for treating or preventing HIV infection comprise first and second T cell specific peptide(s) with one peptide having a sequence derived from HIVp17gag protein
            09-AUG-1996;
                                                                                                                                                                                                                              HIV p17 gag protein antigenic peptide HIV-1TB132.
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                                           08-AUG-1997;
                                                                         19-FEB-1998.
                                                                                                                                   Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                             21-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                             AAW55845;
                                                                                                                                                                                                                                                                                                                           AAW55845 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                p17 gag protein; T cell
immune response; HGP-30.
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| 12 cvhqkie 18
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71.4%;
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Pred. No. 1.6e+02;
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peptide having a sequence derived from HIVp17gag protein

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The present sequence represents an HIV p17 gag protein antigenic peptide species specific sequence from the present invention. The peptide species specific sequence from the present invention describes a conjugated peptide which is capable of eliciting a HII response when administered to a human. The conjugated peptide comprises a first T cell specific binding peptide (SBP), and a second T cell SBP, the first and second peptides being derived from different molecules and covalently linked together, where the first T cell SBP binds to a specific class or subclass of T cells the second T cell SBP is an antigenic peptide capable of eliciting THI associated antibodies and having sequence identity with the p17 gag protein of HIV where the peptide has a sequence originating with an amino acid residue chosen from residues 106 to 111 of p17 gag protein of HIV the peptides can induce a THI, TH2 or mixed TH17H2 directed immune resonce anainer and the second are induced a THI, TH2 or mixed TH17H2 directed immune
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                                                                                                 New conjugated peptide(s) for treating or preventing HIV infection comprise first and second T cell specific peptide(s) with one peptide having a sequence derived from HIVp17gag protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                               response against HIV and HIV infected cells. They can be used for treating or preventing HIV infection and AIDS.
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                      Disclosure; Page 10; 58pp; English.
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Best Local Similarity 71.4
Matches 5; Conservative
 (CELS-) CEL-SCI CORP.
                                                                   WPI; 1998-159280/14.
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                                   Sarin PS,
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New conjugated peptide(s) for treating or preventing HIV infection comprise, first and second T cell specific peptide(s) with one

Zimmerman DS;

Sarin PS,

WPI, 1998-159280/14.

(CELS-) CEL-SCI CORP.

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The present sequence represents an HIV p17 gag protein antigenic peptide species specific sequence from the present invention. The present invention describes a conjugated peptide which is capable of eliciting a FHI response when administered to a human. The conjugated peptide comprises a first T cell specific binding peptide (SBP), and a second T cell SBP, the first and second peptides being derived from different molecules and covalently linked together, where the first T cell SBP binds to a specific class or subclass of T cells and the second T cell SBP is an antigenic peptide capable of eliciting and the second T cell SBP is an antigenic peptide capable of eliciting repreted antibodies and having sequence identity with the p17 gag protein of HIV where the peptide has a sequence originating with an amino acid residue chosen from residues 75 to 82 and ending with an amino acid residue chosen from residues 106 to 111 of p17 gag protein of HIV. The peptides can induce a THI, TH2 or mixed THI/TH2 directed immune response against HIV and HIV infected cells. They can be used for treating or preventing HIV infection and AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; human immunodeficiency virus; antigen; conjugated peptide; p17 gag protein; T cell specific binding peptide; TH1; TH2; AIDS; immune response; HGP-30.
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Pred. No. 1.6e+02;
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                                    Disclosure; Page 10; 58pp; English.
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71.4%;
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Best Local Similarity 71...
5; Conservative
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12 cvhqkie 18
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AAW55851
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RESULT
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23-MAR-1999;
28-MAY-1999;
The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage lambda; att; recombination site; attB; attP; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the first T cell SBP binds to a specific class or subclass of T cells and the second T cell SBP is an antigenic peptide capable of eliciting TH1 associated antibodies and having sequence identity with the p17 gag protein of HIV where the peptide has a sequence originating with an amino acid residue chosen from residues 75 to 82 and ending with an amino acid residue chosen from residues 106 to 111 of p17 gag protein of HIV. The peptides can induce a TH1, TH2 or mixed TH1/TH2 directed immune response against HIV and HIV infected cells. They can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cohjugated (SBP), and
                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2000; 2000WO-US05432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage
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                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
                                                                                                                                                                Example
                                                                                                                                                                                                recombinational cloning of
                                                                                                                                                                                                                                                                                                                            (LIFE-) LIFE
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les 5; Conser
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                                                                                                                                                                4; Fig 14; 459pp; English
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                                                                                                                                                                                                                                                                                             Brasch
                                                                                                                                                                                                                                                                                                                            TECHNOLOGIES INC
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99US-0126049.
99US-0136744.
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                                                                                                                                                                                                                                                                                             Temple GF,
                                                                                                                                                                                               polypeptides
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Pred.
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No. 1.6e+02;
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Best Local S
Matches 5
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                                             useful in the treatment of blood coagulation disorders, e.g. thrombosis, etc. It is also useful in the study of phosphatidylserine which plays an important role in the cell membrane, artificial
                                                                                         The sequence is that of a peptide recognising phosphatidyl-serine and ethanolamine. It inhibits the activity of blood coagulation factor VIII, and does not inhibit the activity of factor V. It is
                                                                                                                                                                                           New physiologically active peptide recognising phosphatidyl-serine and-ethanolamine - inhibits activity of blood coagulation factor VJ but not factor V, used for treating thrombosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphatidylserine recognising peptide
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Sequence
                                                                                                                                                            Claim 2;
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treatment;
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5; Conserv
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                                  and medicinal artificial material.
   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity; blood coagulation artificial membrane; medicin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                            2; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                     91JP-0276138
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Pred.
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2.5e+02;
6;
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Query Match Best Local S Matches 6

Similarity 6; Conserv

Conservative

0 Score Pred.

Mismatches

Indels

0;

Gaps

0

No.

2.le+02; DB

Length 13;

14 RQKVEGS 20 || || || || 2 rqnvegs 8 oy D

Search completed: July 19, 2001, 07:47:34 Job time: 45 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match Length
   July 19, 2001, 07:46:49; Search time 12.2 Seconds (without alignments) 34.675 Million cell updates/sec
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107
1 VIDHQGTKSSKCVRQKVEGSS
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/ACTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
   BB
US-08-564-063-25
US-08-564-063-3
US-08-564-063-3
US-08-695-301A-18
US-08-695-301A-21
US-08-695-304C-18
US-08-695-304C-24
US-08-695-304C-24
US-08-695-304C-24
US-08-695-304C-28
US-08-695-304C-28
US-08-695-304C-28
US-08-695-304A-29
US-08-695-301A-16
US-08-695-301A-16
US-08-695-301A-29
US-08-695-301A-23
US-08-695-301A-29
US-08-695-301A-33
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 Sequence
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                     3, Appli
3, Appli
3, Appli
3, Appli
24, Appl
28, Appl
28, Appl
28, Appl
29, Appl
30, Appli
30, Appli
31, Appli
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31, Appli
31, Appli
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	US-09-179-558-17	US-08-840-006-4	US-08-871-355A-290	US-08-637-759B-290	US-08-429-964-75	US-08-908-526-5	US-08-695-304C-34	US-08-695-304C-33	US-08-695-304C-32	US-08-695-304C-31	US-08-695-304C-29	US-08-695-304C-27	US-08-695-304C-23	US-08-695-304C-22	US-08-695-304C-20	US-08-695-304C-19	US-08-695-304C-16	US-08-695-301A-34
•	Sequence 17, Appl	Sequence 4, Appli	Sequence 290, App	Sequence 290, App	Sequence 75, Appl	Sequence 5, Appli	Sequence 34, Appl	Sequence 33, Appl	Sequence 32, Appl	Sequence 31, Appl	Sequence 29, Appl	Sequence 27, Appl		Sequence 22, Appl	Sequence 20, Appl		Sequence 16, Appl	•

# ALIGNMENTS

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LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-564-063-25
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US-08-564-063-25
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                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,063
FILING DATE: 28-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, Paula A
REFIGERICE/DOCKET NUMBER: 37.03
REFERENCE/DOCKET NUMBER: FRD-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                      TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SAKARIASSEN, KJell S
APPLICANT: STEPHENS, ROSS W
APPLICANT: ORNING, Lars
APPLICANT: ORNING, LARS
TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault, LLP
STREET: 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 125 H
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110
                   3 DHQGTKSS 10
2 DHTGTKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08564063
                                                                                                                                                                                                                                                             9 amino acids
                                                                        Conservative
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                                                                                       29.9%;
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Pred. No. 1.4e+05;
                                                                        Mismatches
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                                                                                                        Length 9;
                                                                      Indels
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Sequence 18, Application US/08695301A
Patent No. 6093400
GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
TITLE OF INVENTION: Compositions and Methods of Use
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.4 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1
CURRBUT APPLICATION NUMBER: US/08/695,301A
FILING DATE: AUGUST 9, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2; Length 11; Pred. No. 24;
SOFTWARE: PC-DOS/MS-DOS
SUFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/564,063
FILLING DATE: 28-MAY-1996
CLASSIFICATION: 514
ATTOREX/AGENT THE STATE OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Law Office of Sherman and Shalloway STREET: 413 N. Washington Street CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TORNEY/Aben An Steinberg NAME: Richard A. Steinberg REGISTRATION UNMBER: 26,58 CELL-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FRA
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CE
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TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.9%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 11 amino acids
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LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-564-063-2
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TOPOLOGY: linear
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APPLICANT: SARARIASSEN, Kjell S
APPLICANT: STEPHENS, Ross W
APPLICANT: ORNING, Lars
TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault, LLP
STREET: 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: SARARIASSEN, Kjell S
APPLICANT: STEPHENS, Ross W
APPLICANT: ORRING, Lars
TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
UNDER OF SEQUENCES: 26
CORRESSENDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Testa, Hurwitz & Thibeault, LLP
STREET: 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/564,063
FILING DATE: 28-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, Paula A
NAME: CAMPBELL, Paula A
REGISTRATION NUMBER: 32,503
REFERENCE/POCKET NUMBER: FRD-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08564063
Patent No. 5962418
                                                                                                                                                                                  Sequence 3, Application US/08564063
Patent No. 5962418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match .
Best Local Similarity 75.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-564-063-3
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US-08-564-063-2
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; OTHER INFORMATION: fragment of p-17 gag protein of ; OTHER INFORMATION: HIV-1MN
US-08-695-301A-21
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/695,301A FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEPHONE: (703) 836-0106
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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Best Local :
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Best Local Similarity
                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage MEDIUM TYPE: 3.5 inch, 1.44 mb storage COMPUTER: Del1 System 210; Intel 80 286 Microprocessor OPERATING SYSTEM: MS DOS 6.22 SOFTWARE: Word Perfect, Version 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: FRAGMENT TYPE:
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                                                                                 12 CVRQKVE 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
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                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                  CVHQKIE 18
                                                                                                                 Similarity
5; Conserv
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413 N. Washington Street
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VENTION: Modified HGP-30 Peptides, Conjugates,
VENTION: Compositions and Methods of Use
EQUENCES: 50
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                     peptide
internal fragment
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71.4%;
                                                                                                                                   29.0%;
                                                                                                                                   Score 31;
Pred. No.
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Pred. No.
                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                             Sequence 28, Application US/08695301A Patent No. 6093400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
COMPUTER: MS DOS 6.22
OPERATING SYSTEM: MS DOS 6.22
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FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS D
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                        APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN TITLE OF INVENTION: modified HGP-30 Peptides, Conjugates, TITLE OF INVENTION: Compositions and Methods of Use NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 549-2282
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FRAGMENT TYPE:
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LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1DYI
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STATE: Virginia
                                                          COUNTRY:
                                                                                              STREET: 413 N. Wa
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                                                                                                                                        ADDRESSEE:
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TOPOLOGY: linear
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                                                          Virginia
Y: USA
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413 N. Washington Street
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VENTION: Modified HGP-30 Peptides, Conjugates,
VENTION: Compositions and Methods of Use
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internal fragment
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9, 1996
  5.25 inch, 1.2 mb storage
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MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 3; Length 20; Pred. No. 69;
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APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
TITLE OF INVENTION: Compositions and Methods of Use
                                                                                                                     LOCATION: 75 to 94
CTHER INFORMATION: fragment of p-17 gag protein of
CTHER INFORMATION: HIV-1TB132
US-08-695-304C-18
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ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
                                                                                                                                                                                                                                                     DB 3;
69;
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Pred. No.
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SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-102
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/08695304C Patent No. 6103239
                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
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FRAGMENT TYPE: internal fragment
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71.4%;
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TELEPAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 71.4.
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                                                                                                             NAME/KEY:
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                             POPOLOGY
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MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210: Intel 80 286 Microprocessor
OPERATIG SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/98/69;301A
FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
RESTRENCE/DOCKET NUMBER: 26,588
REFERENCE/DOCKET NUMBER: 26,588
REFERENCE/DOCKET NUMBER: 26,588
REFERENCE/DOCKET NUMBER: 26,588
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 836-0106
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage MEDIUM TYPE: 3.5 inch, 1.44 mb storage COMPUTER: Dell System 210; Intel 80 286 Microprocessor OPERATING SYSTEM: MS DOS 6.22 SOFTWARE: Word Perfect, Version 5.1 APPLICATION DATA: APPLICATION NUMBER: US/08/695,304C FILLING DATE: August 9, 1996 ATTONNEY/AGENT INFORMATION:
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Patent No. 6103239
GENERAL INFORMATION:
APPLICANT: DANNEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
TITLE OF INVENTION: Compositions and Methods of Use
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: fragment of p-17 gag protein of OTHER INFORMATION: HIV-1HAN
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STATE: Virgin:
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internal fragment
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REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CEI
TELECOMMUNICATION INFORMATION:
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71.4%;
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TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 18
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Best Local Similarity 71.4
S. Conservative
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COMPUTER READABLE FORM:
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LOCATION: 75 to 94
                                                                                                                                                                                                                                                                                                                                                      amino acid
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: USA
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MOLECULE TYPE:
FRAGMENT TYPE:
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12 CVHQKIE 18
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US-08-695-304C-18
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US-08-695-304C-28
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Best Local Similarity
5; Conserve
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; LOCATION: 75 to 94
; OTHER INFORMATION: fragment of p-17 gag protein of p-17 gag protein of p-18 gag protein of p-18 gag protein of p-18-695-304C-24
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US-08-695-304C-24
                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                          Sequence 28, Application US/08695304C Patent No. 6103239 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/08695304C Patent No. 6103239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 549-2
TELEFAX: (703) 836-010
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/695,304C
FILING DATE: AUGUST 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-102
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage MEDIUM TYPE: 3.5 inch, 1.44 mb storage COMPUTER: Dell System 210; Intel 80 286 Microproc OPERATING SYSTEM: MS DOS 6.22 SOFTWARE: Word Perfect, Version 5.1 CURRENT APPLICATION DATA:
                                                                                               APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN TITLE OF INVENTION: Modified HGP-30 Heteroconjugates, TITLE OF INVENTION: Compositions and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN TITLE OF INVENTION: Modified HGP-30 Heteroconjugates, TITLE OF INVENTION: Compositions and Methods of Use NUMBER OF SEQUENCES: 56
                                                         CORRESPONDENCE ADDRESS
                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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FRAGMENT TYPE:
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STATE: Virginia
COUNTRY: USA
                      ADDRESSEE:
STREET: 4
                                                                                                                                                                                                                                                                                                                                          12 CVRQKVE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 20 amino
TYPE: amino acid
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SEE: Law Office of Sherman and Shalloway
: 413 N. Washington Street
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Law Office of Sherman and Shalloway 413 N. Washington Street
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
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internal fragment
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) 836-0106
- NO: 24:
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                                                                             Compositions and 56
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71.4%;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/US94/04496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.0
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 70, Appli Patent No. 6040140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 836-01 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
COMPUTER: MS DOS 6.22
COPPUTATION SYSTEM: MS DOS 6.22
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FILING DATE: AUGUST 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 549-2282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: V
COUNTRY:
                                                                                                                                                                                                                                                                                      ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz ADDRESSEE: Wo. 6040140ris STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                               STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: · 22314
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GY: linear
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internal fragment
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                                                                                                                                                                                                                                                                                                                                                                                                              Resulting from Chromosome Abnormalities in the All-1 Region
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71.4%;
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    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Scott, John D.,
APPLICANT: Muert, Brian J.,
APPLICANT: Klauck, Theresa M.
APPLICANT: Klauck, Theresa M.
APPLICANT: ROUNENTION: Protein Binding Domains of Gravin NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5: Marshall, O'Toole, Gerstein, Murray 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/769,309A
                                                                                                                                                                                                                                                                                                                                                                           DB 5;
62;
                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: NO. 5741890and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.1%; Score 29; Best Local Similarity 50.0%; Pred. No. 9 Matches 6; Conservative 3; Mismatch
                                                                                                                                                                                                                                                                                                                                                                              Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            TJU-1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/08769309A; Patent No. 5741890
                                                                                   REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ. ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                      33,229
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TELEPHONE: 312-474-6300
                        ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-04496-70
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                                                                                                                                                                                                                                               amino acid
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      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-769-309A-6
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US-08-769-309A-6
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GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
ADDRESSEE: Noris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30;
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-CCT-1994
PRIOR APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
                                                                                                                                                                                                                                                                                                 PALON PROMER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: PCT/US92/10930
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TJU-1262 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.0%;
63.6%;
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Best Local Similarity 63.6
Matches 7; Conservative
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ATTORNEY_AGENT INFORMATION:

NAME: NO. 6090929and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/33451

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-648

TELEFAX: 312-474-0448

TELEY 25-3856

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE: CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

US-08-994-570-6
Search completed: July 19, 2001, 07:47:09 Job time: 20 sec
                                                                                                             В
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US-08-994-570-6
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Patent No. 6090929
GENERAL INFORMATION:
APPLICANT: Scott, John D.,
APPLICANT: Nauert, Brian J.,
APPLICANT: Klauck, Theresa M.
TITLE OF INVENTION: protein Binding Domains of Gravin
NUMBER OF SEQUENCES: 24
CORRESSORDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                           Query Match 27.1%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1:30
CURRENT APPLICATION DATA:
OURSING APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/994,570 FILING DATE: CLASSIFICATION:
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CITY: Chicago
STATE: Illinois
                                                                                                        7 TKSSKCVRQKVE 18
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3 TKSSKLVQNIIQ 14
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 19, 2001, 07:49:39; Search time 12.68 Seconds (without alignments) . 30.037 Million cell updates/sec

Title: Perfect score: Sequence: US-08-487-283A-1\_COPY\_8\_12 27 1 KSSKC 5

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Searched:

Total number of hits satisfying chosen parameters:

205

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	<sub>5</sub>	4	ω	2	1	NO.	Result	
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29.6	9	9	9	9	9	9	ω	۳	Ψ	ω	ω.	Ψ	ω	ω	ω	w	ω.	33.3	ω	ω	7.	7.	7.	7	7	7.	7.	37.0	Match I		dР
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branched-chain-ami	T-cell receptor be	T-cell receptor be	T-cell receptor be	-	l receptor	1 receptor	T-cell receptor be		T-cell receptor be	T-cell receptor be		Ig heavy chain CRD		R-phycoerythrin ga	R-phycoerythrin al	major protein anti	Ig mu chain V regi	metallothionein-A	hypothetical prote		receptor		T-cell receptor be	hemoglobin, extrac	lari	ndi	idi	T-cell receptor be	Description		

RESULT

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# ALIGNMENTS

vative 1; Mismatc	platelet aggreg	SULT 2 5238 11idipin - a	Query Match Best Local Similarity 66.7%; Pred. No. 2.2e+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 2 SSK 4 I ASK 3	J. Exp. Med. 174, 115-124, 1991 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A;Reference number: PT0509; MUID:91277601 A;Accession: PT0534 A;Status: translation not shown A;Molecule type: mRNA A;Residues: 1-4 <fee> A;Experimental source: adult thymus, strain BALB/c C;Keywords: T-cell receptor</fee>	RESULT 1 PT0534 T-cell receptor beta chain V-D-J region (126-1AC) - mouse (fragment) C; Species: Mus musculus (house mouse) C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 C; Accession: PT0534 R; Feeney, A.J.

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R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A;Reference number: PT0509; MUID:91277601
A;Accession: PT0577
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J. Exp. Med. 174, 115-124, 1991
A.Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions A; Feference number: PT0509; MUID:91277601
A; Accession: PT0565
A; Status: translation not shown
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0700
                                                                                                          T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0700
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Pred. No. 2.2e+05;
1; Mismatches 0; Indels
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Pred. No. 2.2e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: day 19 fetal thymus, strain BALB/c, A;Accession: PT0574
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A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992
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66.7%;
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ilarity 66.7%;
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Best Local Similarity 66.7-
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Best Local Similarity
Matches 2; Conserv
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A; Residues: 1-5 <FEE>
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A; Residues: 1-5 <FE2>
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2 SSR 4
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C;Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accession: B45522
R;Wesseling, JG.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmak Mol. Biochem. Parasitol. 35, 167-176, 1989
A;Title: Stage-specific expression and genomic organization of the actin genes of the ma A;Reference number. A45525; MUID:89364996
A;Accession: B45525
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May.1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: A33882
C;Accession: A33882
C;Accession: A33882
R;Jackson, P.J; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(qamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant A;Reference number: A94182; MUID:88016144
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actin I - malaria parasite (Plasmodium falciparum) (fragments)
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Pred. No. 2.2e+05;
1; Mismatches 0; Indels
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A) Cross-references: GB:J03988
A) Note: the authors translated the codon GAA for C; Comment: The actin I gene contains no introns.
                          downy thornapple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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A33882
cadmium-binding pentapeptide
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A;Molecule type: protein
A;Residues: 1-5 <FUS>
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Best Local Similarity
Matches 1; Conserv
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Matches 1; Conserv
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RESULT
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Eur. J. Biochem. 188, 505-510, 1986
A; Title: A transcription terminator in the
A; Reference number: I40503; MUID:86274732
A; Accession: I40505
                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 3 (4 aa) - Bacillus stearothermophilus C;Species: Bacillus stearothermophilus C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change C;Accession: I40505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites
A;Reference number: A22565; MUID:85182601
A;Accession: A22565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment) C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
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A22565
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A;Molecule type: DNA
A;Residues: 1-5 <FEE>
              metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
C;Accession: I51049
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  R;Olsson,
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R; Nagai, S; Wiker, H.G.; Harboe, M.; Kinomoto, Infect. Immun. 59, 372-882, 1991
A;Title: Isolation and partial characterization A;Reference number: A60274; MUID:91099989
A;Accession: D60274
                                                                                                                                                                                                                                                                                                                                                                       major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: D60274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice A;Reference number: S43956; MUID:94248036 A;Accession: S43959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision
C;Accession: S43959
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A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss)
A;Reference number: I51049; MUID:95324545
A;Accession: I51049
B22565
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A; Residues: 1-4 <WAG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1;
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A;Molecule type: DNA
A;Residues: 1-4 <OLS>
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R-2040 Coerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
R-phycocrythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C,Dete: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C,Accession: F22565
R,Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A,Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A,Recession: F22565
A,Molecule type: protein
A,Residues: 1-5 <KLO>
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993 C;Accession: B22565 R;Klotz, A.V.; Glazer, A.N.
B;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A22565; MUD:85182601 A;Recession: B22565 A;Molecule type: protein A;Residues: 1-5 <KLO>
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:51:09 ; Search time 9.96 Seconds (without alignments) 17.197 Million cell updates/sec

Title: Perfect score: Sequence: US-08-487-283A-1\_COPY\_8\_12 27

1 KSSKC 5

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters:

28

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result NO: 1 2 3 4 5 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Query Match Le 29.6 25.9 25.2 22.2 22.2 18.5 18.5 18.5 14.8 14.8 14.8 14.8 17.4 7.4 7.4 7.4	Length DB		BIOB CITER TRM3_ECOLI TRM3_ECOLI TRM3_ECOLI TRM3_ECOLI TRM3_ECOLI TUFT_HUMAN TUFT_HUMAN GRWM_HUMAN
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ALIGNMENTS

RESU TRM33 AC DT TRM3 OC GN DT TRM3 OC GN CC	2 H O	HESCO CCC CCC CCC CCC CCC CCC CCC CCC CCC
LET 2  JECOLI  TRM3_ECOLI  STANDARD; PRT; 5 AA.  P13973;  01-JAN-1990 (Rel. 13, Cereated) 01-JAN-1990 (Rel. 13, Last sequence update) 17-AN-1990 (Rel. 37, Last annotation update) 15-DEC-1998 (Rel. 37, Last annotation update) 17-AM PROTEIN (FRAGMENT).  TRAM  Escherichia coli.  Plasmid IncFII R100.  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.  NCBI_TaxID-562; [1]  SEQUENCE FROM N.A.  SECHETIAL TaxID-562; [1]  SEQUENCE FROM N.A.  SECHETIA	ery Match 29.6%; Score 8; DB 1; Lenst Local Similarity 100.0%; Pred. No. 9.3e+04; tches 2; Conservative 0; Mismatches 0; 2 SS 3   1   4 SS 5	OB_CITER STANDARD; PRT; 5 AA.  P12997;  O1-JAN-1990 (Rel. 13, Created)  O1-JAN-1990 (Rel. 13, Last sequence update)  O1-CCT-2000 (Rel. 40, Last annotation update)  D1OTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).  Citrobacter freundii.  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  Citrobacter.  NCBL_TaxID=546;  E1]  SEQUENCE FROM N.A.  MEDLINE-89006280; PubMed=2971595;  Shiuan D., Campbell A.;  "Transcriptional regulation and gene arrangement of Escherichia coli,  Citrobacter freundii and Salmonella typhimurium biotin operons.";  Gene 67:203-211(1988).  -1- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) - BIOTIN.  -1- PATHHAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHHAY.  -1- PATHHAY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES  FAMILY.  FAMILY.  FAMILY.  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute of Bioinformatics and the EMBL outstation on the suse by and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)  EMBL, M21922: -, NOT_ANNOTATED_CDS.  Biotin biosynthesis; Iron-sulfur; Transferase.  NON_TER 5 A; 532 MM; 75A5B1EDD6F00000 CRC64;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ol-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN (EC 1.2.99.2) (FRAGMENT).
Bacteria; Proteobacteria.
NOBL_TaxID=290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90055678; PubMed-2818128;
Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carboxyddrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR - CO(2) + REDUCED
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io. 9.3e+04;
0; Indels
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                                                                                                                                                                                                                                                                                                                                             Length 5;
                                                                                                                                                                                                                                                                               5 AA; 634 MW; 6B1B1AA443500000 CRC64;
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                                                                                                                                                                                                                                                                                                                                        25.9%; Score 7; DB 1; L4
25.0%; Pred. No. 9.3e+04;
tive 2; Mismatches 1;
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21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT 2000 (Rel. 40, Last annotation update)
PHACOCYTOSIS-STIMULATING PEPTIDE (TUFFSIN)
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.2%; Score 6; DB 1
50.0%; Pred. No. 9.36
live 1; Mismatches
                                                                                                                                                                                      EMBL; M20941; -; NOT_ANNOTATED_CDS.
PIR; A32014; A32014.
Conjugation; Plasmid; DNA-binding.
NON_TER
SEQUENCE 5 AA; 634 MW; 6B1B1AA4
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Oxidoreductase; Molybdenum.
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 1; Conserv
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1 KNDE 4
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P19918;
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SEQUENCE
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MEDLINE-68091045; Pubmed-4169272;
Fidalgo B.V., Najjar V.A.;
Fidalgo B.V., 
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                                       Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Schlesinger D.H., Pickart L., Thaler M.M.;
Schlesinger D.H., Pickart L., Traiper B.G.,
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
Experientia 33:324-325(1977).
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SEOUENCE 3 AA; 340 MW; 6331E8100000000 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
GROWTH-MODULATING PEPTIDE.
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Pred. No.
MEDLINE=72187087; PubMed=4112769;
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50.0%;
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SEQUENCE
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21-JUL-1986 (Rel. 01, Last
21-JUL-1986 (Rel. 01, Last
EOSINOPHILOTACTIC PEPTIDES.
                                                                                                                                  anaphylaxis.";
                                                                                                                                                         human lung tissue: identification
                                                                                                                                                                         MEDLINE-76078412; PubMed-1060093;
Goetzl E.J., Austen K.F.;
"Purification and synthesis of eosinophilotactic
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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Bacteria; Proteobacteria;
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01-MAR-1992 (Rel. 21, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
LONG-CHAIN-FATTY-ACID--LUCIFERIN-COMPONENT LIGASE
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te for the lux operon.";
Bacteriol. 172:6797-6802(1990).
- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
- IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
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new Vibrio fischeri lux gene precedes
                                                                                         MISCELLANEOUS: THE
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    EOSINOPHILS, OF ENZYMES,
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MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SH
                                                                                                                                                                                                                                                                                                                                                            sapiens (Human)
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01, Last annotation updat
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Pred. No. 9.3
0; Mismatches
                                                                                                              72:4123-4127(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meighen
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). 9.3e
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P36515;
O1-JUN-1994 (Rel. 201-JUN-1994 (Rel. 201-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypotensive agent; Venom.
MOD_RES 1 1
SEQUENCE 5 AA; 629 MW;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence up
01-FEB-1994 (Rel. 28, Last annotation
BRADYKININ-POTENTIATING PEPTIDE S5,2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90351557; PubMed-2386615;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
"Primary structure and biological activity of bradykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BPP7_BOTIN P30425;
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VARIANT
Grohmann L.,
                    SEQUENCE.
MEDLINE=91285106;
                                                                           NCBI_TaxID=4932;
                                                                                               Eukaryota; Fungi; 
Saccharomycetales;
                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                     YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tides from Bothrops insularis snake venom.";
Protein Chem. 9:221-227(1990).
FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
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G37196; G37196
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  Graack H. -R.,
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29, Last a
RIBOSOMAL
                                                                                               Ascomycota; Saccharomycotina; Sacci; Saccharomyces
                    PubMed=2060626;
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                                                                                                                                                                         Last sequence upday, Last annotation upon process and profess L1 (
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6B05B862A0000000 C
  Kruft V.,
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776DC37326B00000
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Pred. No. 9.3e
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Pred.
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  Choli T.,
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9.3e+04;
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9.3e+04;
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    Goldschmidt-Reisin S.,
                                                                                                                    Saccharomycetes;
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Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.
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Matches 0; Conserv
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=602;
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01-NOV-1995
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P12678;
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P42562;
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FAR3_HIRME
ID FAR3_H:
AC P42562,
DT 01-NOV-DT
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BIOB_SALTY
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Kitakawa M.;
"Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.";
FEBS Lett. 284:51-56(1991).
PIR; S17255; S17255.
SGD; L0002681; MRPL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROFRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.8%; Score 4; DB 1; Length 5; llarity 100.0%; Pred. No. 9.3e+04; Conservative 0; Mismatches 0; Indel.
                                                                                                                            Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide; Amidation; Multigene family.

MOD_RES 5 5 AMIDATION (POTENTIAL).

SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
                                                                                         4 AA; 402 MW; 7771B2D5D000000 CRC64;
                                                                                                                                                                                                                                                                                                                 Carcinus maenas (Common shore crab) (Green crab).
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                           DB 1; Le
                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 14.
                                                                                                                                                                                                                                                  5 A.A.
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                                                                                                                          14.8%; Score 4; DB 1
100.0%; Pred. No. 9.3
iive 0; Mismatches
                                                                                                                                                                                                                                                   PRT;
                                                                   Ribosomal protein; Mitochondrion.
                                                                                                                            14.8%;
                                                                                                                          Query Match 14.8
Best Local Similarity 100.
Matches 1; Conservative
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Matches 1; Conserv
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P81817;
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P38005;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-89066280; PubMed-2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli, citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-! CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
-! - PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
-! - SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                                                                                                                                                                                                                                                                                       Gaps
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-0cT-1989 (Rel. 12, Last sequence update)
01-0cT-2000 (Rel. 40, Last annotation update)
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).
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Pallini V.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF
PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER 5 5 SEQUENCE 5 AA; 611 MW; 7761F40DD6F00000 CRC64;
                                                                                                                                           SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;
                                                                                                                                                                                                                             14.8%; Score 4; DB 1; Lei 100.0%; Pred. No. 9.3e+04; ative 0; Mismatches 0;
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Pred. No. 9.3e+04;
2; Mismatches C
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StyGene; SG10027; bioB.
Biotin biosynthesis; Iron-sulfur; Transferase.
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(Rel. 32, Last sequence update)
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Best Local Similarity
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FAR4_HIRME
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P42561;
01-NOV-1995
01-NOV-1995
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                                                                                                                                                                                                                                                                                        Neuropeptide; Amidation.
MOD_RES 4 4
SEQUENCE 4 AA; 616 MW;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE YMRF-AMIDE.
Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail). Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                          FLRFAMIDE.
                                                                                                                                                                                                                                                                                                                                            MEDLINE=92195954; PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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Evans B.D., Pohl J., Kartsonis M.A., Cala
"Identification of Rramide neuropeptides
Peptides 12:897-908(1991).
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Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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69D4073B30000000
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Pred. No. 9.3e+04;
1; Mismatches
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1; Mismatches
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[2]
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                                                                                                                                                                                 SPECIES-H.trivolvis; TISSUE-Kidney; MEDLINE-94286417; PubMed-7912428; Madrid K.P., Price D.A., Greenberg
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SPECIES=H.medicinalis;
MEDLINE=92195954; Pubm
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MOD_RES
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"FMRPamide-related peptides from the kidney
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Search completed: July 19, 2001, 07:53:50 Job time: 161 sec

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Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
Biochem. FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
                                                                                                                                                                                                                                                                                                                        MEDLINE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last seq)
01-JAN-1999 (TYEMBLrel. 09, Last ann
UDP-GLUCURONOSYLTRANSFERASE, MICROSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium; Multigene family.
NON_TER 5 5
SEQUENCE 5 AA; 600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aleurone layers.";
Plant Mol. Biol. 16:713-721(1991).
Plant Mol. Biol. 16:713-721(1991).
-:- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
-:- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-:- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Control of transient expression of chimaeric acid and abscisic acid in protoplasts prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
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                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=GUNN;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91329704; PubMed=1831055; Jacobsen J.V., Close T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HIMALAYA; TISSUE-ALEURONE LAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
                                                                              Transferase;
                                                                                                                                  <del>:</del>
                                                                                                                                                                             -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                                                                                                                           BETA-D-GLUCORONOSIDE.
SUBCELLULAR LOCATION:
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                                                                                                                                                                                                      ENDOGENOUS COMPOUNDS.
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                                                                                                    S38636; AAB19259.1;
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1; Conserv
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     MW:
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                                                                                                                             MICROSOME
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     633732C420000000 CRC64
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Last annotation update)
, MICROSOMAL (EC 2.4.1.17) (UDPGT)
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Pred.
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Sciurognathi; Muridae;
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; Murinae; Rat
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Query Match

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626 MW;
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Best Local Similarity
'-hag 0; Conserve
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NCBI_TaxID=104895;
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nes 0; Conserv
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                            5 AA;
        Amphibian skin.
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-! FUNCTION: CABEIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
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Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: CARRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
                              Gaps
                                                                                                                                                                                                                                                                                                                       Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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-!- MASS SPECTROMETRY: MW-598; METHOD-FAB.
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Last annotation update)
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          Pred. No. 4.2e+05;
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Pred. No. 4.2e+05;
1; Mismatches (
100.0%; Prea. ....
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                          1; Conservative
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Best Local Similarity 0.0%
Matches 0; Conservative
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        Best Local Similarity
Matches 1; Conserv
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SEQUENCE 5 AA
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Litoria
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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-1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
-1- MASS SPECIFOMETRY: MW-655; METHOD-FAB.
Amphibian skin; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing Litori electrica. Comparison with the skin peptides from rubella.";
                                       Indels
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Length
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 3.2.
                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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5 AA; 656 MW; 71A9C9CB10300000 CRC64;
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Pred. No. 4.2e+05;
1; Mismatches 0
                Pred. No. 4.2e+05;
1; Mismatches (
DB 13;
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Score 1;
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nilarity 0.0%; P
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                0.0%;
                                   Conservative
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RRITAR COCCOCCATA
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P82099
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Best Local S
Matches
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Best Local
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P82100;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                   P82099; PRELIMINARY;
P82099; OTEMBLES 1
01-MAY-2000 (TIEMBLES 1
01-MAY-2000 (TIEMBLES 1
01-MAY-2000 (TIEMBLES 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
SEQUENCE.
TISSUE=SKIN SECRETION;
TRISSUE=SKIN SECRETION;
Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing
"Peptides from with the skin peptides from the 
                             SEQUENCE. SECRETION:
TISSUE-SKIN SECRETION:
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian bu
Litori electrica. Comparison with the skin peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aust. J. Chem. 52:0-0(1999).

-!- FUNCTION: CABRIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.

-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
Amphibian skin.
SEQUENCE 5 AA; 570 MW; 71A9C9C862A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                       rubella."
                                                                                                                                                                NCBI_TaxID=104895;
                                                                                                                                                                                                                     Litoria rubella (Desert tree frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                         ELECTRIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amphibian skin; Amidation.
MOD_RES 5 5
SEQUENCE 5 AA; 616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=104895;
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                                                                                                                                                                                                        Amphibia; Batrachia;
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                                                                                                                                                                                       Litoria
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J. Chem. 52:0-0(1999).
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13,
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61F2D1A059A00000 CRC64;
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Pred. No.
1; Mismat
                                                                                                                                                                                                           Neobatrachia;
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Pred. No. 4.2e+05;
1; Mismatches
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4.2e+05;
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Search completed: July 19, 2001, 07:53:34 Job time: 165 sec
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Best Local S
Matches
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MOD_RES
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nilarity 0.0%;
Conservative
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668761F2C9A00000 CRC64;
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Pred. No. 4.2e+05;
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Minimum
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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27
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res

CD8 activation com	AAB37555	22	5	59.3	16	11
Thrombin-induced p	AAB72592	22	<sub>5</sub>	59.3	16	10
Thrombin-induced p	AAB72577	22	σ	59.3	16	9
LI-cadherin cell a	AAY63087	21	5	59.3	16	8
Peptide motif of S	AAY83309	21	5	63.0	17	7
IL-1 antagonist pe	AAB17208	21	ر ن	66.7	18	6
CD8 activation com	AAB37548	22	5	81.5	22	σ
Human chemokine de	AAB15855	21	5	81.5	22	4
Human chemokine PF	AAB15838	21	5	81.5	22	w
Chemokine peptide,	AAY14251	20	ر د	81.5	22	2
Chemokine peptide,	AAY14283	20	5	81.5	22	٦
Description	ID	DB	Query Match Length	Query	Score	No.
				æ		
	SUMMARIES					

45	44	43	42	41	40	39	38 .	37	36	ω 5	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16 .	15	14	13	12	
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AAW88040	AAW88038	AAY30280	AAW43234	327	AAW43278	AAW43277	27	AAW43275	7	AAW43273	AAW43272	~	AAW43270	AAW43269	AAW43268	AAW43267	113		AAY20407	AAW15187	5	AAR36658		AAY51896	AAY64348	AAY63614	AAW65315	AAW67231	AAW77359	AAR77331	143	33	AAB12055	
Peptide used in th	c	grin	ide #11	#56	#55	ide #54	#53	#52	ide #51	ide #50	ide #49	ide #48	#47		ide #45	ide #44	ide 13 u	Peptide 13 used to	Human microtubule	Chelating moiety f	icrobial tet	Η	-	Biostatin TT232 sy	Cadherin-related n	ein c	Peptide #7. Synth	unoreactiv	mIL-10 C-terminal	Human apolipoprote	Matrix metalloprot	metallopro	G4 GTPase motif fr	

## ALIGNMENTS

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AAY14283
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                 vasculitis; lentiviral infection; low bone mineral density; suppressor; parasitic infection; autoimmune disease; psoriasis; wound healing; organ transplant rejection; rheumatoid arthritis; allergy; therapy;
                                                                                                                                                                                                                                                      Chemokine; immune response; monocyte chemoattractant protein-1; MCP-1; chemokine-induced activity; inflammatory response; vascular indication; haematopoietic cell-associated activity; tumour; coronary artery disease; myocardial infarction; unstable angina pectoris; atherosclerosis; asthma;
         Grainger DJ,
                                                                                                                                                               Synthetic.
                                                                                                                                                                                                      organ transplant
arachidonic acid
                                                                                                                                                                                                                                                                                                                      Chemokine peptide, LFL peptide2(6-10)[MCP-1].
                                                                                                                                                                                                                                                                                                                                               29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                        AAY14283;
                                    (NEOR-) NEORX CORP.
                                                             11-SEP-1997;
                                                                                      11-SEP-1998;
                                                                                                               18-MAR-1999.
                                                                                                                                        W09912968-A2
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                AAY14283 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                         ۲
                                                                                                                                                                                                                                                                                                                                              (first entry)
          Kanaly ST,
                                                             97US-0927939
                                                                                      98WO-US19052
                                                                                                                                                                                                      pathway.
           Tatalick LM;
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Tatalick LM;

Kanaly ST,

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New chemokine peptides and mimetics
                           WPI; 1999-347124/29
  Grainger DJ,
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                                                                                                                                                      cell-associated activity at a tumour site. They can also be used for preventing an inhibiting an indication associated with haematopoietic cell recruitment or histamine release from basophils or mast cells. They can also be used to modulate the chemokine-induced activity of haematopoietic cells at a preselected physiological site, to treat a vascular indication, e.g. coronary artery disease, myocardial infarction, unstable angina pectoris, atherosclerosis, or vasculitis, lentiviral infection or replication (e.g. HIV), low bone mineral density, a parasitic infection in a vertebrate animal (e.g. malaria), an autoimmune treat psoriasis in a mammal, to enhance wound healing, to prevent or treat asthma, organ transplant rejection, rheumatoid arthritis or the arachidonic acid pathway and where leukotriene, thromboxane and/or prostation as inhibited and to prevent or inhibit an indication crostaglandin are inhibited and to prevent or inhibit an indication associated with elevated TNF-alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemokine; immune response; monocyte chemoattractant protein-1; MCP-1; chemokine-induced activity; inflammatory response; vascular indication; haematopoietic cell-associated activity; umour; ocronary artery disease; myocardial infarction; unstable angina pectoris; atheroscierosis; asthma; vasculitis; lentiviral infection; low bone mineral density; suppressor; parasitic infection; autoimmune disease; psoriasis; wound healing; organ transplant rejection; rheumatoid arthritis; allergy; therapy; arachidonic acid pathway.
                                                                            This sequence represents a fragment of the chemokine MCP-1. The invention relates to chemokine peptides and mimetics, particularly derived from monocyte chemoattractant protein-1 (MCP-1). The chemokine peptides and variants and derivatives on inhibit or reduce or increase, or enhance chemokine-induced activity. They can be used for increasing or enhancing an inflammatory response, an immune response or haematopoietic
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~~d. No. 3.4e+05;
0; Indels
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                           New chemokine peptides and mimetics
                                                     Disclosure; Fig 14; 208pp; English
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WPI; 1999-347124/29
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Best Local Similarity
Matches 4; Conserv
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This sequence represents a fragment of the chemokine hMCP-1.

The invention relates to chemokine peptides and mimetics, particularly derived from monocyte chemotizatant protein-1 (MCP-1). The chemokine peptides and variants and derivatives can inhibit or reduce or increase, or enhance chemokine-induced activity. They can be used for increasing or enhancing an inflammatory response, an immune response or haematopoietic cell-associated activity at a tumour site. They can also be used for preventing or inhibiting an indication associated with haematopoietic cell recruitment or histamine release from basophils or mast cells. They can also be used to modulate the chemokine-induced activity of haematopoietic cells at a preselected physiological site, to treat a vascular indication, e.g. coronary artery disease, myocardial infarction, constable angina pectoris, atheroselecosis, or vasculitis, lentiviral infection or replication (e.g. HIV), low bone mineral density, a infection in a vertebrate animal, to prevent or treat psoriasis in a mammal. To enhance wound healing, to prevent or treat asthma, organ transplant rejection, rheumatoid arthritis or allergy. They can also be used to inhibit a product or intermediate in the arachidonic acid pathway and where leukotriene, thromboxane and/or prostaglandin are inhibited and to prevent or inhibit an indication conservated mith elevated TNF-alpha.
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Disclosure; Page 10; 208pp; English
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17-MAR-1999;
01-DEC-1999;
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Best Local S
Matches 4
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New peptide 3, amide and heterocyclic compounds and saccharide conjugates used for inhibiting chemokine induced activity and treating e.g. stroke, vascular diseases, autoimmune diseases a
                                                                                                              (NEOR-)
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17-MAR-1999;
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                                                                                                                                                                                                                                                                                                               rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                           basophil-mediated disease; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                      monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV; AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia
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                                                                                                                                        99US-0229071.
99US-0271192.
99US-0452406.
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100.0%; Pred. No.
tive 0; Mismatc
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3.4e+05;
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  diseases and tumour
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20-AUG-1999;
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                               detrimental cytotoxic T lymphocyte responses. These compounds mimic or interact with a surface feature (such as SHN, KIT, SSK, DEK and RDT) of the CD8/MHCI complex. This is useful in meno +harmonic transfer.
                                                                                                  Disclosure;
                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                         CD8 activation complex; cytotoxic T lymphocyte response; analogu surface feature; gene therapy; diabetes; tissue transplantation.
                                                                                                                                                     Composition for inhibition of detrimental cytotoxic T lymphocyte
                                                                                                                                                                                                                            (PHIL-) PHILADELPHIA HEALTH & EDUCATION CORP
                                                                                                                                                                                                                                                                                                        02-MAY-2000; 2000WO-US11902
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                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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99US-0150150.
99US-0162632.
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100.0%; Pred. No.
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3.4e+05;
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Sequence diabetes

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and

in tissue transplantation.

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Length 5;

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(L1)C-P1-(L2)d-P2-(L3)e-P^3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently selected that expendently expensive of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a b, c, d, e, and f = are each independently linkers; and a b, c, d, e, and f = are each independently linkers; and an b, c, d, e, and f = are each independently linkers; and a b, c, d, e, and f = are each independently linkers; and a b brown of interesting cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein contains complement fixation, and possibly placental transfer. AAA69443 co AAAA69526 and AAB16955 to AAB18013 represent invention.
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                                             Gaps
                                                                                                                                                                                                                                                                                 Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                             ö
                 Length 5;
             81.5%; Score 22; DB 22; Length 5; 100.0%; Pred. No. 3.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         IL-1 antagonist peptide sequence SEQ ID NO:264
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                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 289; 608pp; English.
                                                                                                                                                                      AAB17208 standard; Peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                             31-OCT-2000 (first entry)
Ouery Match
Best Local Similarity luv...
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
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                                                                      2 SSKC 5
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                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel recombinant DNA molecules encoding subtilisin-like serine protease, useful for producing transgenic plants with altered stomata, lower water consumption and enhanced diseased resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences encoding SDD1, a subtilisin-like serine protease, can be used to produce transgenic plants with altered stomata characteristics. These plants exhibit improved freshness, increased ary weight, reduced leaf temperatures, reduced water loss and lower water consumption and for enhancing the sugar and/or protein content of plant leaves, modulating CO_2 uptake into and H_20 release from leaves, for sustained photosynthesis under high intensity conditions or for the improvement of disease resistance of plants. The transgenic plants and cells of such plants are useful in the preparation of feed, food or additives.
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  SDD1; serine protease; subtilisin; transgenic plants; dry weight; stomata; sugar; water; protein; CO_2; H_2O; CO2; H2O; crop protection; feed; foodstuffs.
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                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                             Peptide motif of SDD1 subtilisin-like serine protease.
DB 21; Le.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
             66.7%; Score 18; DB 100.0%; Pred. No. 3.4
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                                                                                                                                                                                                                                                              AAY83309 standard; Peptide; 5 AA.
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llarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98EP-0119244.
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
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                                Local Similarity
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Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                 16-AUG-2000
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                                                                                                     1 KSSK 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                          AAY83309;
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                                         Best Loca
Matches
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                                                                                                                                                                                                                                       AAY83309
                                                                                                                                                                                                                    RESULT
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AAY63087 RESULT

Sequence

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05-MAY-1998;
06-NOV-1998;
20-JAN-1999;
                            blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diapnosis and in bioreactors. AAY60592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY6453 and AAZ33183 to AAZ33186 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                              inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cadherin related neuronal receptor; LI-cadherin; protocadherin;
desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
                                                                                                                                                                                                                                                           angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
expressing cell, preventing or treating obesity in a mammal, stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OB-cadherin;
cadherin-12;
                                                                                                                                                                                                                                                                                                                                                                  recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.
                                                                                                                                                                                                                                                                                                                                                                                    comprising peptides which comprise a nonclassical cadherin celrecognition (CAR) sequence. The MAs can be used for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blaschuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1999;
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes cadherin modulating agents (MA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell
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cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gour BJ,
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98US-0187859.
99US-0234395.
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                                                                                                                                                                                                                                                                                                                                                                                            activation in a human cell expressing protease activated receptor 1 (PARI). The method involves using peptides (e.g. the present peptide) that inhibit platelet activation. The method is useful for preventing thrombosis and platelet aggregation. The method can be used for patiently the contraction of the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used for patiently agree that the method can be used to the method can be used to be used to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting thrombin activation in human cell expressing protease activated receptor 1 (PAR1), comprises contacting mixtures of thrombin and human cell expressing PAR1, with a peptide that inhibits platelet
                                                                                                                                                                                                                                                                                                                    with acute coronary syndromes (e.g. cresendo angina, myocardial infarction) and for individuals who have acute coronary syndromes and receive percutaneous transluminal coronary angioplasty with an artificle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for inhibiting thrombin activation in a human cell expressing protease activated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Platelet aggregation inhibitor; thrombin activation inhibitor; protease activated receptor 1; PAR1; platelet activation inhibitor;
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                              stent placement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                   Local Similarity
nes 2; Conserv
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                                                                                                         Conservative
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                                                                                                                               Score 16; DB 22;
Pred. No. 3.4e+05;
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Pred. No. 3.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                          for patients
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                                                                                                         Gaps
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RESULT 10
AAB72592
ID AAB72
XX

AAB72592 standard; Peptide;

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The present invention provides compositions which can be used to inhibit detrimental cytotoxic T lymphocyte responses. These compounds mimic or interact with a surface feature (such as SHN, KIT, SSK, DEK and RDT) of the CD8/MHCI complex. This is useful in gene therapy, in the treatment of diabetes and in tissue transplantation.
                                                                                                                                                                                                                                             Composition for inhibition of detrimental cytotoxic T lymphocyte responses comprising a compound that mimics or interacts with a surface feature of the CD8/MHC I complex -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease; cell proliferation; cell differentiation; tissue repair; transcription regulator; breast cancer; gene therapy; melanoma; neuroblastoma; leuvedraemia; Parkinson's disease; Huntingdon's disease; Alzheimer's disease; paralysis; motor neurone disorder; 64 GTPase motif; EF-Tu/ Ha-RAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.3%; Score 16; DB 22; Length 5; 50.0%; Pred. No. 3.4e+05; ive 2; Mismatches 0; Indels
                                                                                                                                   (PHIL-) PHILADELPHIA HEALTH & EDUCATION CORP.
                                                                                                                                                                                                                                                                                                                        Disclosure; Page 35; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G4 GTPase motif from EF-Tu/ Ha-RAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB12055 standard; Peptide; 4 AA.
                   02-MAY-2000; 2000WO-US11902.
                                                        99US-0132361
99US-0150150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0516859
                                                                                              99US-0162632
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95US-0399411
                                                                                                                                                                          Jameson BA, Tretiakova A;
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Matches 2; Conserv
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06-MAR-1995;
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                                                        04-MAY-1999;
20-AUG-1999;
                                                                                              01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for inhibiting thrombin activation in a human cell expressing protease activated receptor 1 (PARI). The method involves using peptides (e.g. the present peptide) that inhibit platelet activation. The method is useful for preventing thrombosis and platelet aggregation. The method can be used for patients with acute coronary syndromes (e.g. cresendo angina, myocardial infarction) and for individuals who have acute coronary syndromes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receive percutaneous transluminal coronary angioplasty with an artificle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting thrombin activation in human cell expressing protease activated receptor 1 (PAR1), comprises contacting mixtures of thrombin and human cell expressing PAR1, with a peptide that inhibits platelet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                            Platelet aggregation inhibitor; thrombin activation inhibitor; protease activated receptor 1; PAR1; platelet activation inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD8 activation complex; cytotoxic T lymphocyte response; analogue; surface feature; gene therapy; diabetes; tissue transplantation.
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Pred. No. 3.4e+05;
1; Mismatches 2; Indels
                                                                        Thrombin-induced platelet activator antagonist #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD8 activation complex RDT ridge analogue SC8-21.
                                                                                                                                                     thrombosis; acute coronary syndrome.
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                                   09-MAY-2001 (first entry)
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                                                                                                                                                                                        Unidentified
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AAB72592;
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New PR domain peptides comprising amino acid sequences from, for example retinoblastoma-interacting zinc finger, or egl-43 proteins, for

WPI; 2000-410879/35

WO200066146-A1

RESULT 11 AAB37555

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09-NOV-2000.

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription. RIZ functions to maintain cells in the G1 phase of the cell cycle, by interacting with Rb through the cr2 domain of RIZ. RIZ protein is a PR domain protein and is present primarily in the cell nucleus. RIZ gene mutations may be implicated in various cancers such as melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be used in gene therapy for these disorders. Since RIZ protein is implicated in cell cycle arrest, inhibition of RIZ activity may be useful in neurodegenerative disorder therapy e.g. for Parkinson's, Huntingdon's or Alzheimer's disease, paralysis or motor neurone disorders, or cardiac disorders e.g. heart disease, where the ability to induce neural cardiac tissue proliferation would be useful. The present
This peptide represents a matrix metalloprotease (MMP) inhibitor peptide of the formula: aa1-aa2-aa3-aa4-C where aa1 and aa4 is R or K; aa2 is K,
                                                                                                                                                                                                                                                                                                                                                                                  Matrix metalloprotease; inhibitor; tissue damage; angiogenesis; arthritis; tumour growth; granulomatous inflammatory condition; metastasis; sarcoidosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTPase motif is found in rat RIZ (AAB12104). RIZ is retinoblastoma (Rb)-interacting zinc finger (RIZ) protein. RIZ is a nuclear phosphoprotein that acts as a cell differentiation factor. RIZ can modulate cell growth by binding to Rb protein, which is involved in regulating cell proliferation. In addition, RIZ can act to regulate the protein control of the regulating cell proliferation. In addition, RIZ can act to regulate the regulating cell proliferation.
                                               Claim
                                                                           Matrix metallo:proteinase peptide(s) - used treating tissue damage caused by activated of
                                                                                                                            WPI; 1990-290458/38
                                                                                                                                                         Krutzsh H,
                                                                                                                                                                                         (USDC )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulating gene transcription and controlling cell proliferation differentiation % \left( 1\right) =\left\{ 1\right\}  .
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les 2; Conserv
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                                               3; Page 41;
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                                            61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is a G4 GTPase motif from EF-Tu/ Ha-RAS. The
                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitor peptide #6
                                                                                                                                                         Stetler-Stevenson
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Pred. No.
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3.4e+05;
                                                                              enzyme
                                                                                          to inhibit enzyme
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Score 15; DB 11; Pred. No. 3.4e+05; 1; Mismatches 2;

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Best Local
                                                 This peptide represents a matrix metalloprotease (MMP) inhibitor peptide of the formula: aal-aa2-aa3-aa4-C where aal and aa4 is R or K; aa2 is K, O or N; aa3 is P, A, G, L, I or V; and C is a cysteine having a free sulphydryl group. The peptides can be used to treat tissue damage caused by activated MMPs, e.g. for treating inappropriate anglogenesis, arthritis, tumour growth, invasion and metastasis and granulomatous inflammatory conditions such as sarcoidosis. Antibodies to the peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q or N; aa3 is P, A, G, L, I or V; and C is a cysteine having a free sulphydryl group. The peptides can be used to treat tissue damage caused by activated MMPs, e.g. for treating inappropriate angiogenesis, arthritis, tumour growth, invasion and metastasis and granulomatous inflammatory conditions such as sarcoidosis. Antibodies to the peptides can be used to detect the MMPs and can distinguish activated from laten
Sequence
                                                                                                                                                          Claim 3; Page 41; 61pp; English.
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                                      can be
                                                                                                                                                                                 Matrix metallo:proteinase peptide(s) - used to inhibit enzyme treating tissue damage caused by activated enzyme
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                                      the MMPs and
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                                                                                                                                                                                                                                                    Stetler-Stevenson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  nhibitor; tissue damage; angiogenesis; antibody;
granulomatous inflammatory condition; enzyme;
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Pred. No.
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                                      can distinguish activated
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3.4e+05;
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AAQ91625 encodes AAR77331 a human/old world monkey apolipoprotein (a) (apo(a)) antigenic peptide. The peptide can be used to raise antiapo(a) antibodies, for use in immunoassays for the detection of apo(a). The DNA sequence can be used as a primer and/or probe for the detection, and quantification of apo(a) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immuno:reactive peptide(s) of apo:lipoprotein - used for prodn. of antibodies and development of immunoassays, for the detection and quantification of apo(a)
                                                                                                                                                                                Human; old world monkey; apolipoprotein (a); apo(a); primer; probe; aptigenic peptide; immunoassay; detection; quantification.
                                                                                                                                                      Human apolipoprotein (a) (apo(a)) antigenic peptide.
                                                                           AAR77331 standard; Peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 26; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Butler SM, Taddei-peters WC;
                                                                                                                                                                                                                                                                                                  94EP-0203653.
                                                                                                                                                                                                                                                                                                                          94US-0266407.
93US-0172461.
                                                                                                                             06-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                (ALKU ) AKZO NOBEL NV.
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N-PSDB; AAQ91625.
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21-DEC-1993;
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                                                                                                    AAR77331;
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55.6%; Score 15; DB 16; Length 5; ilarity 75.0%; Pred. No. 3.4e+05; Conservative 1; Mismatches 0; Indels

Query Match Best Local Similarity Matches 3; Conserv

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Search completed: July 19, 2001, 07:50:45 Job time: 166 sec

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Result
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Maximum DB seq length: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_AA:*
1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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Match
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 ,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-07-694-983-2
US-08-243-082-23
US-08-249-568-41
US-08-399-411-41
US-08-399-411-41
US-08-399-820-102
US-08-329-820-103
US-08-329-820-103
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US-08-329-820-103
US-08-329-820-103
US-08-329-820-103
US-08-329-820-103
US-08-915-189-90
US-08-915-189-90
US-08-915-189-90
US-08-915-189-90
US-08-948-193-36
US-08-948-193-36
US-08-95-913-26
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                 Sequence
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   Sequence
                                     2, Appli
41, Appl
41, Appl
41, Appl
41, Appl
34, Appl
102, App
103, App
108, Appl
34, Appl
34, Appl
36, Appl
37, Appl
38, Appl
39, Appl
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31, Appl
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32, Appl
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34, Appl
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37, Appl
38, Appl
39, Appl
30, Appl
30
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Qy 1 KSSK 4       Db 1 KSSK 4	Query Match  Best Local Similarity 100.0%; Pred. No. 1  Matches 4; Conservative 0; Mismatche	INFORMATION FOR SEQUENCE CHARA LENGTH: 4 a TYPE: AMING STRANDEDNESS TOPOLOGY: 1 MOLECULE TYPE: MOLECULE TYPE:	FILING DATE: 19910503  FILING DATE: 19910503  CLASSIFICATION: 530  ATTORNEY/AGENT INFORMATION: NAME: MUTAShige, Kate H. REGISTRATION NUMBER: 29,959 REGISTRATION NUMBER: 9500-0039.00  TELECOMMUTCATION INFORMATION: TELEPAX: 415-327-7250  TELEFAX: 415-327-2951  TELEFAX: 706141	COUNTER: USA ZIP: 94025 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:	NUMBER OF ENVENTION: DISTRIBUTE OF SEQUENCES: 19  CORRESPONDENCE ADDRESS: ADDRESSEE: Irell & Manella STREET: 545 Middlefield Road, Suite CITY: Menlo Park CITY: California	RESULT 1 US-07-694-983-2 ; Sequence 2, Application US/07694983 ; Patent NO. 5432260 ; Patent NO. 5432260 ; GENERAL INFORMATION: ; APPLICANT: Stahl, Philip D. ; TITLE OF INVENTION: HIGH AFFINITY MANNOSE ; TITLE OF INVENTION: LIGHTONE	ALIGNMENT	28 14 51.9 4 1 US-07-694-98 29 14 51.9 4 1 US-08-234-60 30 14 51.9 4 1 US-08-244-49 31 14 51.9 4 2 US-08-244-49 32 14 51.9 4 6 51.68050-9 34 14 51.9 5 1 US-08-234-60 35 14 51.9 5 1 US-08-199-77 36 14 51.9 5 1 US-08-234-60 37 14 51.9 5 1 US-08-18-27 38 14 51.9 5 2 US-08-244-49 39 14 51.9 5 2 US-08-24-49 40 14 51.9 5 2 US-08-718-27 41 14 51.9 5 2 US-08-718-27 42 14 51.9 5 2 US-08-772-72 43 14 51.9 5 2 US-08-772-72 44 14 51.9 5 2 US-08-722-25 45 14 51.9 5 3 US-08-722-25
	DB 1; Length 4; 1.4e+05; nes 0; Indels 0; Gaps 0			ion #1.25	200	SE RECEPTOR	vs	983-3 Sequence 3, Appli -983-4 Sequence 4, Appli -983-4 Sequence 7, Appli -986-5 Sequence 5, Appli -986-47 Sequence 47, Appli -986-47 Sequence 8, Appli -986-8 Sequence 8, Appli -986-8 Sequence 35, Appli -986-8 Sequence 35, Appli -986-2 Sequence 27, Appli -986-71 Sequence 5, Appli -986-71 Sequence 71, Appl -986-71 Sequence 71, Appl

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Score 15; DB 2; Length 4;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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ZIP: 92122
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
FILING DATE: O-MAR-1995
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-UN-1995
CLASSIFICATION: 514
PRIOR APPLICATION: 514
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Patent No. 5831008
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Inte
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
COMPANDERSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 amino acids
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STATE: California
COUNTRY: HSA
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US-08-459-568-41
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-399-411-41
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                                                                                                                                                 Sequence 23, Application US/08243082
Patent No. 5506120
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, HIROAKI
APPLICANT: YAMASHITA, Kunihiko
TITLE OF INVENTION: METHOD OF PRODUCING PEPTIDES OR
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20036
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/243,082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%; Score 18; DB 1; I
100.0%; Pred. No. 1.4e+05;
iive 0; Mismatches 0;
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Patent No. 5811304
GENERAL INFORMION:
TITLE OF INVENTION: Retinoblastoma Protein
TITLE OF INVENTION: 21nc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
PREDEIGTON DUMBER: US/07/853,754
FILING DATE: 05-UNW-1992
ATTORNEY/AGENT INFORMATION:
NAME: Schneller, John W.
REGISTRATION NUMBER: 26,031
REFERENCE/DOCKET NUMBER: 26,031
REFERENCE/DOCKET NUMBER: KUWAT 0010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer, Frank & Schneider
STREET: 1111 Nineteenth Street, N.W.
CITY: Mashington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-243-082-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
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                                                                                      RESULT 2
US-08-243-082-23
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US-08-459-568-41
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US-08-363-475-13
Sequence 13, Application US/08363475
Patent No. 5516679
GENERAL INFORMATION:
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Best Local Similarity
"-+>hes 2; Conserv?
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Matches
                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Zinc Finger Proteins
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
APPLICANT: Chiang, Shu-Jen
                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La
CITY: San Diego
                                                                                                                                                                              Local Similarity 66.
                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SKC 5
                                                                                                                     1 NKC
                                                                                                                                                3 SKC 5
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                                                                                                                                                                                                                                                                                   amino acid
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                               (619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                     linear
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66.7%;
                                                                                                                                                                           55.6%; Score 15; DB 3; 66.7%; Pred. No. 1.4e+05; tive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retinoblastoma Protein - Interacting
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Pred. No. 1.
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                                                                                                                                                                                                         Length 4;
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US-08-456-840-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Taddei-Peters, W.
APPLICANT: Butler, Sandra M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (609) 252 452
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,840
FILING DATE: 01-UN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,661
REFERENCE/DOCKET NUMBER: ON
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 23-DEC-199
CLASSIFICATION: 435
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Savitsky, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas R. Savitsky
STREET: P.O. Box 4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PENICILLIN V AMIDOHYDROLASE GENE FROM TITLE OF INVENTION: FUSARIUM OXYSPORUM NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                            STREET: 1330 Pic
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U. ZIP: 08543
                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           ZIP: 20850
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                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                      ADDRESSEE:
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1330 Piccard Drive
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                                                                                                                                                                                                                                                                                                                                          Taddei-Peters, W. C.
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Pred. No. 1.4e+05;
1; Mismatches 0
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COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993
ATTONEY/AGENT INFORMATION:
NAME: Hamlet King, Diana
REGISTRATION NUMBER: 33,302
RESPERENCE/DOCKET NUMBER: MERCK 1635
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                    Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 103, Application US/08329820
Fatent No. 5747457
GENERAL INFORMATION:
APPLICANT: JONCZYK, ALFRED
APPLICANT: DIFFERMACH, BEATE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors;
NUMBER OF SEQUENCES: 228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    Score 15; DB 1; Pred. No. 1.4e+05;
                                                            /product= "Lys(BOC)"
/note= "N-terminal: FMOC"
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/note= "S-trityl"
                                                                                                                                                                                                                CCATION: 4

OTHER INFORMATION: /product= "Asp(OBut)"
US-08-329-820-102
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                     NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /product= "Thr(But)"
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ilarity 40.0%;
Conservative
               NAME/KEY: Modified-site LOCATION: 1 OTHER INFORMATION: /prod OTHER INFORMATION: /note
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TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: YES
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COTHER INFORMATION:
US-08-329-820-103
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Best Local Similarity
2; Conserve
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GENERAL INCORMATION:

APPLICANT: FELDING-HABERMANN, BRUNHILDE
APPLICANT: DIEFENBACH, BERAL
APPLICANT: DIEFENBACH, BERAL
APPLICANT: RIPPARANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION NUMBER: DE 4336758.5
FILING DATE: 28-CCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
RECISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1635
TELECOMMUNICATION INFORMATION:
MELEPHONE: 703-243-6333
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 1; Length 5;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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OTHER INFORMATION: /product= "Cys-trityl"
OTHER INFORMATION: /note= "S-trityl"
               FILING DATE: 27-JUN-1994
APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: GORmley, Mary E.
REGISTATION NUMBER: 34,409
TELECOMMUNICATION:
TELEPHONE: 301-258-5200
US 08/266,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 102, Application US/08329820
; Patent No. 5747457
; GENERAL INFORMATION:
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75.0%;
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                                                                                                                                                              TELEPHONE: 301-258-5200
TELEFAX: 301-977-0847
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.6
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                 LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
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APPLICATION NUMBER:
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                                                Query Match
Best Local
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Best Local
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INPORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE 4:
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                              Local Similarity nes 2; Conserv
                                                                                                                        NAME/KEY: modified-site
LOCATION: 5
OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /product= "Boc-Lys(Boc)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 27-OCT-1994
                                                                                                                                                                                       OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                     OTHER INFORMATION: /product-
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
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                                                                                                                                                                                                                      NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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 1 KSSKC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KTADC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KSSKC 5
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o. 5747457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JONCZYK, ALFRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                  N-terminal
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                                             55.6%;
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                              Score 15; DB 1;
Pred. No. 1.4e+05;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 1;
Pred. No. 1.4e+05;
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                                                                                                                           "Cys(Trt)"
                                                                                                                                                                                       "Asp(OBut)"
                                                                                                                                                                                                                                                       "Thr(But)"
                                                             Length 5;
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                                Indels
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US-08-266-407A-34
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                                                                                                                                                                                                      Sequence 34, Appli
Patent No. 5874544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/08266407A Patent No. 5786156
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
                                                                                                                        APPLICANT: Taddei-Peters, W. APPLICANT: Butler, Sandra M. TITLE OF INVENTION: Immunore NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 301-258-5200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Taddei-Peters, W. C. APPLICANT: Butler, Sandra M. TITLE OF INVENTION: Immunoreact NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/OFFILING DATE: 27-JUN-1994 CLASSIFICATION: 435
                COUNTRY: U
ZIP: 20850
                                             CITY: Rockville
STATE: Maryland
                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gormley, Mary E REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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1 KTADC
                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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3; Conserv
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                                                                            E: Akzo No. 587454
1330 Piccard Drive
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                                                                                                                                                                         Taddei-Peters, W. C.
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER: US 08/172,461
21-DEC-1993
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75.0%;
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Pred. No. 1.4e+05;
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Length 5; Indels

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Length 5;
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APPLICANT: Livant, Donna L
TITLE OF INVENTION: Anticancer Compounds and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,189
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
                                                                                                                                                                                                      Score 15; DB 2;
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 3
Pred. No. 1.4e-
1; Mismatches
                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: CARTOIL, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UM-02877
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 90:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-894-173-36
; Sequence 36, Application US/08894173A
; Patent No. 6090612
                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 90, Application US/08915189; Patent No. 6001965; Patent No. 6001965 6001955
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                                                                                      not relevant
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                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-915-189-90
                                                                                                                        ; MOLECULE TYPE: peptide US-08-814-567A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 220 Montgome
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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                                                                                                        linear
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                                                                                                        TOPOLOGY:
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US-08-915-189-90
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APPLICANT: ANGLADE, EDDY
APPLICANT: AUGLAVAN, DANIEL M.
APPLICANT: SULLIVAN, DANIEL M.
APPLICANT: ILAROGRELLE, WILLIAM
TITLE OF INVENTION: IMMUNOADHESINS AND METHODS OF PRODUCTION
NUMBER OF INVENTION: AND USE THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 3033-1811

COMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURREMY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.6%; Score 15; DB 2; 75.0%; Pred. No. 1.4e+05 Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: SELBY, ELIZABETH
REGISTRATION NUMBER: 38,298
-REFERENCE/DOCKET NUMBER: 14014.0214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: NEEDLE & ROSENBERG, P.C. 127 PEACHTREE STREET, NE
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/266,407
FILING DATE: 27-UN-1994
APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08814567A Patent No. 5998598 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              NAME: GORMLEY, MARY E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-258-5200
TELEFAX: 301-977-0847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 301-977-0847
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                              CLASSIFICATION:
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STATE: GEORGIA
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US-08-814-567A-6
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Gaps

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GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: Adenylate cyclase and uses therefor
FILE REPERENCE: P14715C
CURRENT APPLICATION NUMBER: US/08/894,173A
CURRENT FILING DATE: 1997-08-13
SOFTMARE: PATOMIC SEQ ID NOS: 97
SOFTMARE: PATOMIC SEQ ID NOS: 97
SOFTMARE: PATOMIC STRANDEDNESS: Single
FEATURE:
ORGANISH Mouse
FEATURE:
OTHER INFORMATION: STRANDEDNESS: Single
FEATURE:
OTHER INFORMATION: MOLECULE TYPE: Peptide
FEATURE:
OTHER INFORMATION: HYPOTHETICAL: NO
OTHER INFORMATION: HYPOTHETICAL: NO
OTHER INFORMATION: ANTI-SENSE: NO
US-08-894-173-36
Query Match
SEST Local Similarity 55.6%; Score 15: DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matchess 2; Conservative 1; Mismatches 0; Gaps 0;
QV 3 SKC 5
Db 1 TKC 3
Search completed: July 19, 2001, 07:51:04
Job time: 135 sec
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
Gen Bmbl:*
1: 9b_ba1:
2: 9b_ba3:
3: 9b_ba3:
4: 9b_in1:
5: 9b_jon:
6: 9b_in3:
6: 9b_on:
8: 9b_pa
11: 9b_pa
11: 9b_p
11: 9
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747
1 ATGGCCGATATCCAGATGAC.....TGGTCACTGTCTCGAGCTGA 747
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_pat2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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111980	AR010133	AR003797	AX006750	A18692	AF329458	AX057943	ID		SUMMARIES
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371 ATGGCTGACATCCAGATGACTCAGTCTCCATCGTCCTTGTCTGCCTCTGTGGGAGACAGA 430
                                                                  GTCACCATCACCTGCGGCGCCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGT
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 1612)
Goshorn, S.C., Graves, S.S., Schultz, J.E., Lin, Y., Sanderson, J.A. and
                                                                                                                                      E31225 Device for
E30616 Antibody an
A63778 Sequence 42
A63772 Sequence 36
A63770 Sequence 32
A63774 Sequence 34
A63774 Sequence 38
A63776 Sequence 40
               AX023363 Sequence
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AX014270 Sequence
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Pred. No. 7.8e-80;
0; Mismatches 242; Indels 9;
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/db_xref="taxon:1895"
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9 AX023363
56 AR132308
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AX023367
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Sequence 3 from Patent WO0075333.
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Best Local Similarity 66.1%;
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2 (bases 1 to 840)
Paul,S., Zhou,Y., Planque,S., Bangale,Y., Nishiyama,Y., Luo,J. and O'Connor-McCourt,M.
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O'Connor-McCourt,M.
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                       241 CAGCCTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTC
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Submitted (18-DEC-2000) Pathology and Laboratory Medicine,
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                                                                                                          GAAGATTTTGCAACTTACTATTGTCAGCGGGCTTACAATA---TGAGGACCTTCGGCCAA
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/trans1_table=11
/product="recombinant single chain Fv antibody"
/prottein_id="AAK09209.1"
/db_xref="GI:12957384"
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/db_xref="taxon:9606"
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/focus
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                         ACCATCACATGTCGAGCAAGTGAGAATATTTACAGTAATTTAGCATGGTATCAACAGAAA 183
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CRASENIYSNLAMYQQKQGKSPQLLVYAATNLADGVPSRESGSGSTQYSLKINSLQS
EDFGSYYCQHFWGTPYTFGGGTKLIKEGGGGGGGGGGGGGGGGGGGGGGQDAELVKPG
ASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPQNDDIXYNEKFKGKATLTAD
KSSSTANWQLNSLTSEDSAVYFCKRSYYGHWGQGTTLTVSSESKYGPPCPSAP"
198 c 214 g 189 t
                                                                                                                                                                                                                                                                                    /product="B72.3 protein single chain
/protein_id="CAA01415.1"
/db_xref="GI:513359"
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<1. .816
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/transl_table=11
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Pred. No. 7.9e-74;
0; Mismatches 220
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                   CTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTT
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Better, M.D., Carroll, S.F. and Studnicka, G.M.
Immunotoxins comprising ribosome-inactivating
Patent: US 5744580-A 89 28-APR-1998;
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Pred. No. 9.1e-71;
0; Mismatches 251;
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/db_xref="taxon:32630"
/note="artificial sequence"
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Sequence 89
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                                                     1 (bases 1 to 723)
Better, M.D., Carroll, S.F. and Studnicka, G.M.
Immunotoxins comporising ribosome-inactivating
Patent: US 5756699-A 89 26-MAY-1998;
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Sequence
AR055339
1 (bases 1 to 723)
Better, M.D., Carroll, S.F. and Studnicka, G.I
Polynucleotides encoding gelonin sequences
Patent: US 5837491-A 89 17-NOV-1998;
                                         Unclassified
                                                              Unknown.
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Pred. No. 9.1e-
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Bernhard, S.L., Better, M.D., Carroll, S.F., Lane, J.A. and Materials comprising and methods of preparation and use ribosome-inactivating proteins patent: US 5416202-A 92 16-MAY-1995;
Location/Qualifiers
                                                                                                                                                                         Score 283.4; DB 10; Length
Pred. No. 9.1e-71;
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                                                                                                                                                                1 GACATCCAGATGACTCAGTCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACT
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63.7%; Pred. No. 9.1e-71;
Live 0; Mismatches 251;
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Location/Qualifiers
                          /organism="unknown"
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                                     ACACTGCCTATTTACAGATCAACAGCCTCAGAGCCGAGGACACGGCTGTGTATTTCTGT
                                                                                           AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC
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Better, M.D., Carroll, S.F. and Studnicka, G.M.
Immunotoxins comprising ribosome-inactivating
Patent: US 5621083-A 89 15-APR-1997;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniaca, ...

Mammalia; Eutheria; Primates; Catarrhini; I

1 (bases 1 to 2871)

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Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.

Heterominibodies

Patent: WO 0006605-A 34 10-FEB-2000;

Patent: WO 0006605-A 34 10-FEB-2000;
                                                                           AACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCC
                                                                                                                                                                                                                                      CCGATATCCAGATGACCCAGTCCCCGTCCTCTCTCGCCTCTGTGGGCGATAGGGTCA
AGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTACAGTGGTTACCCGTACACGTTCG
                  AGCCTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCG
                                                                                                                                                         AGTCAGGTGCCTCCCCAAACTCTGGATTTATAGCACATCCAACTTGGCTTCTGGAGTCC
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BAEUERLE PATRICK A (DE) ;
BIOMEDIZINIS (DE)
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STAYMOLSSLTSEDSAVYCARWDYWGOGTTVTWSSGTPLKDTTHTSGKPLDGEKETL
QIRGREREEMFRELNEALELKDAOAGKEPGGSGGGSTQVCTGTDMKLRLPAS PETHL
DMLHLYGGCQVYQGNLELTYLFTNASLSFLQDIQEVQGYVLIAHMQVRQYPLQRLRI
VRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSLTELKGGVLIGRNP
QLCYQDTILWKDIFHKNNQLALTLIDTNNSRACHPCSPMCKGSRCWGESSEDCQSLTR
TVCAGGCARCKGPLFTDDCCHEQCAAGCTGPKHSDCLACLHENHSGICELKPALVTYN
TDTFESMPNPEGRYTFGASCVTACPYNYLSTDVGSGTLVCPLHNQEVTAEDGTQRCEK
CSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLDESTOGDPASNTAP
LQPEQLAVFETLEEITGYLY ISAMPDSLPDLSVPQNLQVTRGRILHHNGAYSTLOGLG
ISWLGLRSLRELGSGLALIHNTHLCFVHTVPWDDLFRNPHQALLHTANRPEDECVGE
GLACHQLCARGHCWGPGPTQCVNCSQFLRGCEVLECRTLQGLPREYVNARHCLPCHP
ECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSGVKPDLSYMPIWKFPDEEGAC
QPCPINCTHSCVULDDKGCPAEQRASPLTSGHHHHH"

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SSSVSSSYLHWYQQKSGASPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSVEAED
AATYYCQQYSGYPYTFGGGTKLEIKGGGGSGGGGSGGGGSQVKLQESGAELVKPGASV
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/db_xref="GI:10183776"
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/db_xref="taxon:9606"
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n. Mismatches 230;
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LMICKSSQSLIYSDNQKNYLAWYQQKPEQSPKLLIYWASTRKGGYPDRFTGSGSGTDF
TLTISSVKAEDLAVYCHQYRYRPFTFGSGTKLEIKRGGGGSGGGGGGGGGGGG
VOLKQSGPELARPGASVKLGCKASGYTFNRYWMQWYKQRPGGLEMTGAIYPGNGDTK
YTQKFKGRATLIADTSSSTAYMQLSSLASEDSAVYYCVFYYGSDDYVMDWGQGTSVT
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Norwich, Norfolk NR4 7UA,
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/transl_table=11
/product="anti-chlorpyrifos-ethyl scFv recombinant
immunoglobulin"
                                                                                                 GACAGGGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGGTGGAT
             CTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTT
                                                CTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAG
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/en,C., Alcocer,M.J.C., Lee,H.A. and Morgan,M.R.A.
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/db_xref="taxon:33630"
/cell_type="hybridoma"
/note="Mus musculus, strain BALB/c"
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Norwich Research Park, Colney Lane, No
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/db_xref="G1:4928297"
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synthetic construct
artificial sequence.
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Doyen,C., Alcocer,M.J.C., In
Functional antibody scFvs at
chlorpyrifos-cHyl
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    /note="pelB"

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196 TGGTACCAGCAGAAACCAGAGCAGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGG 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAGCAGTCTGCAGCCTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTTGACTTTCGGACAGGGTACCAAGGTGGAAATAAAAC------GTACTGGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGGTGCTTCTGGTGGCGGTGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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                                                                                                            /note="kappa light chain variable region"
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                                                              terminal FLAG sequence"
                                                                                                                                                                                                       478. .837
/note="heavy chain variable region"
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245 g 220 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 262; DB 56;
Pred. No. 1.3e-64;
0; Mismatches 250;
                                                                                                                                                                               /note="artificial linker"
VSSASGAQFEQKLISEEDL
                                                                                                                                                                                                                                                                                                                      /note="c-Myc
212 c
                                                                   /note="amino
76. .417
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.1%;
Best Local Similarity 62.6%;
Matches 478; Conservative
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 GTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAGCCAGGGG
                                                                                                                                                                                                    CTCGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGC
                                                                                                                                CTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGAC
                                                                                                                                                                                                                                                                             CTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                         CCGATATCCAGATGACCCAGTCCCCGTCCCTCTCCGCCTCTGTGGGCGATAGGGTCA
                                                        AGGGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTGCTCTGGTGGCGGTGGATCTG
                                                                                                          CTGAAGATTTTGCTACTTTTTTTTCTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCC
                                                                                                                                                                                                                                                        CAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGGAATCCGGGGTCCCCTG
                                                                                                                                                                                                                                                                                                                               CCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAAC
                                                                                                                                                                                                                                                                                                                                                                 CCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAAC 124
                                                                                                                                                                                                                                                                                                                                                                                                        CCGAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCA 153
                                     AAGGGACACGACTGGACATTCAA-----GGAGGAGGAGGATCAGGTGGTGGTGGTAGCG
                                                                                                                                                                                 ACCGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGC
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Sequence
AX023365
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KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DRE
BABUERLE PATRICK A (DE) ; BORSCHERT KATRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOMEDIZINIS (DE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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ARSPSBSTQPWEHVNAIQEARRULNLSRDTAAEMNETVEVISEMEDLQEFTCLQTRLE
LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIP
FDCWEPVQEHHHHHH
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LSCAASGFTFSSYGMHWVRQAFGKGLEWAVLISYDSSUKYYABSYKGRFTISRDNSKN
TLYLQMNSLRAEDTANYYCAKDMGWGSGWRPYYYYGHDVWGQGTTVTWSGGTFLADTH
HTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
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/db_xref="GI:10183778"
/tans1ation="McMSCIILFLVATATGVHSELQMTQSPSSLSASVGDRVTITCRA
SQSISSYLNMYQQKPGQPPKLLIYMASTRESGVPDRFSGSESGTNYTLTISSLQPEDF
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/db_xref="taxon:9606"
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RIN (DE); MICROMET GES
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Query Match Best Local S Matches 419

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 0006605-A 38 10-FEB-2000;
KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE)
BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1630)
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LSCAASGFTESSYGMHWYQAFGKGLEWVAVLSYDGSNKYYADSVKGRRTISRDNSKN
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                 PTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL
EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF
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                                                                                                        TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGSA
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/db_xref="GI:10183780"
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Submitted (23-FEB-1996) Z. C. Chen, Botany, Univ. of Leicester,
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                   154 CCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAAC
                                      CTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTT
                                                  CTCGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGC
                                                                                          CTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGAC
                                                                                                                                                                                AAGGGACACGACTGGACATTCAA-----GGAGGAGGAGGATCAGGTGGTGGTAGCG
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR synthesized gene from mouse hybridoma
SCR 40"
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FGGGTKLEIRADAAPVYSIFPPSSPGGGGSGGGGSGGGGSVDQVQQPGAELVRSGA
SVKMSCKASGYTFTSYNMHWYQTPGGLEWIGYIYPGNGGTIYNQKFKGKATLTADT
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/transl_table=11
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AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC
                                                  GCTACTAGCTACAACCAGAATTTCAAGGACAAGGCCAGCTTGACTGTAGATAAGTCCTCC
                                                                   AGCACCGAATATACCGAAAATTTTAAAAGACCGTGTTACTATGACGCGTGACACTTCGACT
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Sequence 3 from patent US 5856140.
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Db 712 CTGGTCACTGTCTC 725

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Mammalla; Eutheria; Primates; Catarrhini;
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National Institutes of Health, Mammalian
Unpublished (1999)
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UI-HF-BLO-add-a-01-0-UI.r2 NIH_MGC_37
IMAGE:3061128 5', mRNA sequence.
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    Contact: Robert Strausberg, Ph.D
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                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                               Homo sapiens cDNA clone
                               Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                 AW406828 UI-HF-BL0
BG506654 601861253
BF976253 602245130
AA301347 EST14279
AV686883 AV686883
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AV688963 AV688963
AV712126 AV712126
BG537798 602566152
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AV696029 AV696029
AV682465 AV682465
AV685127 AV695127
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                                                                                                                                                                                                                                                                                                                   BG537031 602565115
AW404507 UI-HF-BL0
BG569796 602590416
BG540787 602570674
BG342083 602463029
BG545408 602572716
BF662874 602144820
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG540224 602569113
BG341239 6025659053
BG535392 6025653053
BG536845 602566383
AW405900 UT-HF-BL0
AW406828 UI-HF-BL0
BG506654 601861253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW405752 UI-HF-BL0
AW405906 UI-HF-BL0
AW391263 QVO-ST021
BG539961 602567476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW405301 UI-HF-BL0
AW406294 UI-HF-BL0
AW406081 UI-HF-BL0
BG548281 602575248
BG341934 602463278
BG341934 602463283
AW404714 UI-HF-BL0
AW406886 UI-HF-BL0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW407904 UI-HF-BL0
AW405753 UI-HF-BL0
AV733319 AV733319
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AW403591 UI-HF-BK0
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AW383563 PM4-HT034
BF975451 602245984
                                                                                   Euteleostomi;
 REFERENCE
AUTHORS
TITLE
                                                                     SOURCE
ORGANISM
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AW405753
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Best Local Similarity
Matches 250; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNT
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Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution informatic found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: Mil Forward.
                                                                                                                                                                                                                                                    GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG
                                                                                                                                                                                                                                                                                                           GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
                                                                                                                                                                                                                                                                                                                                                               CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGCAGCTCTGCAGCCT 246
                                                                                                                                                                                                                                                                                                                                                                                                    GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 202
                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
I Homo sapiens
Eukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 493)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                                                                                                                                                                                      GGGACCAAGGTGGAAATCAAACGAACTGTGGGTGCACCATCTG
                                                                                                                                                                                                                                                                                           GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 142
                                                                                                                                      AW405753 493 bp mRNA EST 16-FEB-2000 UI-HF-BL0-abp-a-02-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057290 5', mRNA sequence.
                                                                                                 EST
                                                                                   human
                                                                                                            AW405753.1
                                                                                                                            AW405753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3061128"
/clone_lib="NIH_MGC_37"
/tissue_type="Lymph"
/cell_type="germinal center B
/cell_line="MCC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (LTI)"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                              GI:6924810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.0%;
72.9%;
                                           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 2.8
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    Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8e-49;
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  Gene Collection (MGC)
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Length

0;

Gaps

0

82

262

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

RESULT AW407904

DEFINITION Snoor

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Oian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
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NIH-WGC http://mgc.nci.nih.gov/.
                                                  Homo sapiens CDNA cdA clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
Tel: 86-21-50801919(ex.45)
Pax: 86-21-50801919
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site_1: sfiIA; Site_2: sfiIB"
t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 AGGTTCAGTGGCAGTGGATCTGGATCAGATTTCACTCTCGCCATCAGCAGTCTGCAACCT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 GACATCCAGATCTCCATCTCCTCTGTTGTGTGGGAGACAGAGTCACC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ATCACCTGCGCCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW405301 487 bp mRNA EST 16-FEB-2000 UI-HF-BLO-ack-b-02-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059259 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 GATATCCAGATGACCCCAGTCCCCGTCCTCCTGTCGCCCTCTGTGGGGCGATAGGGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 GGGACCAAGGTGGAAGTCAAACGAACTGTGGCTGCACCATCTGG 437
                                                                                                                                                                                                                           Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 188.8; DB 3.
Pred. No. 1.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pheochromocytoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pTriplEx2;
192 c 171 g 143
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cdAACE02"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="cdA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW405301.1 GI:6924358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.3%; 71.8%;
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Best Local Similarity 71.8
Matches 247; Conservative
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: prit3-pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (L5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 680)
Yang,Y., Song,H., Peng,Y., Gu,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV733319 648 bp mRNA EST 17-OCT-2000
AV733319 cdA Homo sapiens cDNA clone cdAACE02 5', mRNA sequence.
AV733319.1 GI:10850864
        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/image.html
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 ATCACCTGCGCGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 189.4; DB 115; Length 493; Pred. No. 9.1e-48; 0; Mismatches 96; Indels 0;
                                                                                                                                                                                                                                                             1. 493
/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="IMAGE:3057290"
/clone=lib="NIH_MGC_37"
/cisue_type="lymph"
/cell_type="garminal center B cells"
/cell_line="mGCB5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B (LTI)"
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72.0%;
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    Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 471)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                        AW406294 471 bp mRNA EST UI-HF-BLO-aco-b-09-0-UI.rl NIH_MGC_37 Homo IMAGE: 3059657 5', mRNA sequence.
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Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution informa
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/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
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AW406081.1
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Mammalia; Eutheria;
1 (bases 1 to 566)
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UI-HF-BLO-acv-h-03-0-UI.rl NIH_MGC_37
IMAGE:3060700 5', mRNA sequence.
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                                                                                               Homo sapiens
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Contact: Robert St
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/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_1: 
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/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
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                                                                                                                                                                                                                                                                                                                                                                /cell_reg_g_g_g_nminal center B cells"
/cell_line="WAC85"
/lab_host="bH10B (LTI)"
/note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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                                                Contact: Robert Strausberg, Ph.D.
Email: GapDs-remail.nlh.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: MI3 Forward.
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 NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.9e-46;
0; Mismatches 99; Indels
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                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3060700"
/clone=INIH_MGC_37"
/tissue_type="lymph"
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BG548281
BG548281.1 GI:13546946
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Best Local Similarity 71.1%;
Matches 244; Conservative (
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/lab_host="DHIOB (TI phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggeccetcagec); Site_2: Sfil (ggeccettatggec); S' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGCGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MC Library."
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BG341934 GI:13148372
                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA541 row: p column: 12
High quality sequence stop: 726.
Location/Qualifiers
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                                1 (bases 1 to 864)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                               cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapb.r-dmail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:4703483"
/clone lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage
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                                                                              GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTG 395
                                                                                                                                             GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAGACGTTCGGCCAA
                                                                                                                                                                                                              CGGTTCAGTGGCAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                             ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                                                             GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG 349
                                                                                                                                                                            GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
                                                                                                                                                                                                                                            CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
                                                                                                                                                                                                                                                                            GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
                                                                                                                                                                                                                                                                                                          GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT
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Plate: L/cM1288 row: g column: 19
High quality sequence stop: 673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G) . Size-selected >500bp for average insert size 1.8kb .Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
242 a 266 c 231 g 217 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4576170"
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Pred. No. 3.4
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGATAGGGTCACC 66
                                                                                                                                                                    GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTG
                                                   GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG
                                                                                                                GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAGACGTTCGGCCAA
                                                                                                                                                                                                                                GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
                                                                                                                                                                                                                                                                                          CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                       GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCACTTGCCGGGCGAGTCAGGGCATTAACAATTTTTTAGCCTGGTATCAGCAGAAACTA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: L/CM1288 row: e column: 21
High quality sequence stop: 616.
Location/Qualifiers
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Clone_lib="NIH_MCC_48"
//tissue_type="primary B-cells from tonsils (cell line)"
//tissue_type="primary B-cells from tonsils (cell line)"
//lab_host="DH10B (phage=resistant)"
//note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA Synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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71.18;
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345 ACCAGACTGGAGATCAAACGAACTGTGGCTGCACCATCTG 384

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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 608)
                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html

Seq primer: Mi3 Forward
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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UI-HF-BLO-acd-c-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058580 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 TTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 115; Length 608;
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Pred. No. 8.1e-46;
0; Mismatches 98; Indels
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/clone=lib="NIH_MGC_37"
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                                                                                                                                                    AW404714.1 GI:6923771
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Best Local Similarity 71.2%;
Matches 242; Conservative
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                                                                                 DEFINITION
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SOURCE
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/Ub_xrief="taxon:9606"
/Clone="IMAGE:3061499"
/Clone="IMAGE:3061499"
/Clone="IMAGE:3061499"
/Closue_11b="NIH_MGC_37"
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/Cell_Lipe="MGCB5"
/Lab_host="NH10B (LTI)"
/Lab_host="NH10B (LTI)"
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/NOCE="Vector: pT773-Pac; Site_1: NOCI: pT773-Pac; Site_1: 
                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Eco Ri site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                      AW406886 431 bp mRNA EST 16-FEB-2000 UI-HF-BL0-adg-h-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone.IMAGE:3061499 5', mRNA sequence.
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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates;
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GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
                                                                                                                                              GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT
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Seq primer: M13 Forward.
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National Institutes of Health, Mammalian
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129 c 111 g 102 t
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/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
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/note="Vector: pT/T3-Pac; Site_1: NotI; Site_2: Eco
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/cell_line="MGC85"
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/db_xref="taxon:9606"
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Pred. No. 8.6e-46;
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                                                                                                                                                                                 ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
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AGGTTCAGTGGCAGTGGATCTGGGGCAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
                                   CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
                                                                                                                       GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
                                                                                                                                                            ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATCTAAATTGGTATCAGCAGAAACCA 164
                                                                                                                                                                                                                                              GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 104
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                                                                                 GGGAAAGCCCCTGAGCTCCTGATCCATGCTGCATCCAGTTTGCAAATTGGGGTCCCATCA 224
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Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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1 (bases 1 to 460)
1 (bases 1 to 460)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Seg primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058847"
/clone=lib="NIH_MGC_37"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DHIOB (LTI)"
/lab_host="DHIOB (LTI)"
/note="Yector: pT/Tr3-Pac; Site_1: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Lou
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

a 128 c 113 g 112 t
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                24.5%;
70.8%;
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                                                                                                                                                                                                                                                                                                                             Score 183; DB 115;
Pred. No. 8.7e-46;
0; Mismatches 100;
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/clone_lib=*NHL MGC_77*
/lab_host="hH10B (T1 phage-resistant)"
/note="logan: lung: Vector: pDNR-LIB (Clontech); Site_l:
/note="logan: lung: lung
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1 (bases 1 to 867)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   151 ACTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAAAAACCAGGG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                          BG539961 867 bp mRNA EST 03-APR-2001
602567476F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4692138
                                                                                                                         10 ATCCAGATGACCCAGTCCCCGTCCTGTCCGCCTCTGTGGGCGATAGGGTCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1512 row: g column: 19
High quality sequence stop: 704.
Location/Qualifiers
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Pred. No. 2.8e-45;
....arthes 99; Indels
                                                                                                                                                                                                             303 ACAGGGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG 349
                                                                                                                                                                                                                                               318 CCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTG 272
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1 250 c 217 g 159 t
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/db_xref="taxon:9606"
/clone="IMAGE:4692138"
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/db_xref="taxon:9606"
/clone_lib="sr0214"
/dev_stage="Adult"
/note="Organ: stromach; Vector: pucl8; Site_1: SmaI;
/note="Organ: stromach; Vector: Pucle by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pucl 8 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-ST0214-
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                AW391263 653 bp mRNA EST 04-FEB-2000
QVO-ST0214-291199-064-d06 ST0214 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
247 GAAGACTICGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                  63 CACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAA 122
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                                                                                                                   307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGCTTCTG 349
                                                                                                                                                  HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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High quality sequence stop: 653
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Minimum DB
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Listing first 45 summaries
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    729.4
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1: /SIDS1/gcgdata/geneseq/geneseqn/Na1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn/Na1981.DAT:*
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4: /SIDS1/gcgdata/geneseq/geneseqn/Na1983.DAT:*
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Humanised CDR-graf
Murine 5G1.1M1 ScF
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RESULT

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AAT08480
        Evans MJ, Matis L, Mueller EE, Rother RP, Springhorn J P, Squi Wang Y, Wilkins JA;
                                                                                                                                                                                            Complement C5; haemolysis; kidney; glomerulonephritts; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR; single chain antibody; scFv; ds.
                                                                  02-MAY-1994;
                                                                                                                                               CDS
                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                             Humanised CDR-grafted 5G1.1 scFv CB DNA.
                                                                                     01-MAY-1995;
                                                                                                         09-NOV-1995.
                                                                                                                           WO9529697-A1.
                                                                                                                                                                                                                                                                15-MAR-1996
                                                                                                                                                                                                                                                                                   AAT08480;
                                                                                                                                                                                                                                                                                                      AAT08480 standard; DNA;
                                               (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                (first entry)
                                                                  94US-0236208
                                                                                      95WO-US05688
                                                                                                                                               Location/Qualifiers
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                 EE, Nye SH,
Squinto SP,
                    Thomas TC;
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                                                                                          DNA (AAT08480) coding for humanised CDR-grafted scFv CB (AAR77607) was derived from DNA of hybridoma ATCC HB 11625, the producer of anti-C5 monoclonal antibody (MAb) 561.1. The DNA was subcloned into vector PET Trc SO5/NI for expression in Escherichia coli. The light and/or heavy chain CDRs of scFv CB can be combined with CDRs from other 561.1-derived antibodies, Fds and light chains (AAR77607-16) in the prodn. of recombinant, including humanised, antibodies that retain the ability of MAb 561.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 tcgactagtacagtatacatggagctctccagcctgcgatcggaggacacggccgtctat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTCTCGCTTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCA
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                                     C5
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                                                                                                                                                                                                                                                                       Length 747;
                                    glomerulonephritis with antibody against complement
                                                                                                                                                                                                                                                                                             Indels
                                                  - to inhibit complement induced cell lysis
                                                                                                                                                                                                                                 Sequence 747 BP; 161 A; 186 C; 209 G; 191 T; 0 other;
                                                                                                                                                                                                                                                                     100.0%; Score 747; DB 16; 100.0%; Pred. No. 1.7e-199;
                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                       Claim 33; Page 110-113; 181pp; English
                                                                                                                                                                                                           associated with glomerulonephritis.
                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 747; Conservative
WPI; 1995-392923/50.
             P-PSDB; AAR77607
                                                  component
                                    Treating
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                  Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA construct (AAT08488) codes for a humanised CDR-grafted scrv, designated 5G1.1 scrv D012 (AAR77616), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned into vector pET Trc SO5/N1 (see AAT08489) for expression of humanised scrv in Escherichia coli MEI cells. Such human complement catain the ability of MAB 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGCCGATATCCAGATGACCCAGTCCCCCTGTCCTCGTCGCGCTTGTGGGCGATAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
                                                                                                                                                                                                                                                                                                                                                                                    Complement C5; haemolysis; kidney; glomerulonephritis; monocolonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR; single cell antibody; scFv; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rollins
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98.5%; Pred. No. 1.5e-194;
iive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EE, Nye SH,
Squinto SP,
                                                                                                                                                                                                                                                                                                                                   Humanised CDR-grafted 5G1.1 scFv DO12 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                     721 ggaaccctggtcactgtctcgagctga
GGAACCCTGGTCACTGTCTCGAGCTGA
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P, Springhorn J P,
Wilkins JA;
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                                                                                                                                                                                                                                                                                 15-MAR-1996 (first entry)
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Best Local Similarity 98.5
Matches 736; Conservative
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                                                                                                                                                                                standard;
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Wang Y, Wi
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KW Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                         Score 371; DB 16;
Pred. No. 2.4e-94;
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                                                                                                                                   A DNA construct (AAT08483) codes for a humanised CDR-grafted and framework sequence-altered Fd 5G1.1 VH + IGHRL (AAR77610), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (AAT08484) coding for a humanised light chain (AAR77612) into vector APEX 3P (AAT08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAD 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                         TATTGCGCGCGTTATTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAA
TCGACTAGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR;
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Thomas TC;
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RP, Springhorn J P, Squinto SP,
Wilkins JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 38; Page 123-125; 181pp; English.
                                                                                                                                                                                                           GGAACCCTGGTCACTGTCTCGAGCTGA 747
                                                                                                                                                                                                                                                                gggaccacggtcaccgtctcctcatga 747
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1..750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised 5G1.1 VH + IGHRLC DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT08484;
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Wang Y,
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Key

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Rollins S; Thomas TC;

EE, Nye SH, Squinto SP,

Evans MJ, Matis L, Mueller Rother RP, Springhorn J P, Wang Y, Wilkins JA;

Sequence 750 BP; 163 A; 220 C; 197 G; 170 T; 0 other;

717

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Best Local :
                                             Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engine humanised antibody; complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA construct (AAT08487) codes for a humanised CDR-grafted light chain, designated SG1.1 VL + IGHRLD (AAR77615), which incl CDRs derived from mouse anti-C5 monoclonal antibody SG1.1. The DNA can be subcloned together with DNA (AAT08484) coding for a humanised Fd (AAR77611) into vector APEX-3P (AAT08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb SG1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
                                                                                                                                                                        AAT08483 standard;
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P-PSDB; AAR77615.
           Synthetic
                                                                                               Humanised 5G1.1 VH + IGHRL
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                                                                                                                                                                                                                                                                                GGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAG 417
                                                                                                                                                                                                                                              CAAGGAACCCTGGTCACTGTCTCGAGC 744
                                                                                                                                                                                                                                                                                                                                GGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtaactgccggcgtccactcccaagtccaactggtgcaatccggcgccgaggtcaagaag 96
                                                                                                                                                                                                                                   caaggaaccctggtcactgtctcgagc
                                                                                                                                                                                                                                                                                                                                                          ACTTCGACTAGTACAGGATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTC
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95.3%;
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                                             engineering;
region; CDR;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
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                                                                                                                                                                                                                                                              GGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAG
CAAGGAACCCTGGTCACTGTCTCGAGC 744
                                 TATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGT
                                                                                                                         GGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGAC
                                                                                                                                                                     gtaactgccggcgtccactcccaagtccaactggtgcaatccggcgccgaggtcaagaag
                                                                            ACTTCGACTAGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r RP,
                      tattattgcgcgcgttatttttttggttctagcccgaattggtattttgatgtttggggt
                                                                  acttcgactagtacagcctacatggagctctccagcctgcgatcggaggacacggccgtc
                                                                                                              ggctctggtagcaccgaatatgcccaaaaattccagggccgtgttactatgactgcggac
                                                                                                                                                                                                                                                                                              364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RP, Springhorn Wilkins JA;
                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matis L,
                                                                                                                                                                                                                                                                                              Conservative
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Squinto S
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Pred. No. 1.6e-88;
                                                                                                                                                                                                                                                                                                                                                   199
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SP,
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67..708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                  Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rother RP, Springhorn J P, Squinto SP, Thomas TC; Wang Y, Wilkins JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - to inhibit complement induced cell lysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 726 BP; 175 A; 206 C; 187 G; 158 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%; Score 328.8; DB 16;
llarity 96.6%; Pred. No. 1.5e-82;
Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 42; Page 129-131; 181pp; English
Location/Qualifiers
                                                                                                                                                                                                                                Humanised 5G1.1 VL + KLV56B DNA
                                                                                                                 BP.
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                                                                                                               AAT10706 standard; DNA; 726
                                                                                                                                                                                            (first entry)
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76..723
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1..75
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Matches, 336; Conserv
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                                                                                                                                                                                          02-APR-1996
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                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                       AAT10706;
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                                        A DNA construct (AAT08486) codes for a humanised CDR-grafted light chain, designated 5G1.1 VL + 012 (AAR77614), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (AAT08484) coding for a humanised Fd (AAR77611) into vector APEX-3P (AAT08476) for
AACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis
                                                                                                                                                                                                                                                                                                                 Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR;
                                                                                                                                                         Rollins S;
Thomas TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EE, Nye SH,
Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 35; Page 132-34; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                              Humanised 5G1.1 VL + 012 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evans MJ, Matis L, Mueller
Rother RP, Springhorn J P,
Wang Y, Wilkins JA;
                                                                                                                                                                                                                                AAT08486 standard; DNA; 711
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Best Local :
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                                                     01-MAY-1995;
                                                                                                                              mat_peptide
                                                                                                                                                   sig_peptide
                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                      Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                         15-MAR-1996
                                                                                                                                                                                                                                                                                                                              AAT08485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 711 BP; 174 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glomerulonephritis.
           (ALEX-) ALEXION PHARM INC
                                02-MAY-1994;
                                                                                                W09529697-A1
                                                                                                                                                                                                                                                                                    Humanised
                                                                                                                                                                                                                                                                                                                                                  AAT08485 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                          GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                              gaagacttcgctacgtattactgtcagaacgttttaaatactccgttgactttcggacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatatccagatgacccagtccccgtcctccctgtccgcctctgtgggcgatagggtcacc 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331;
                                                                                                                                                                                                                                                                                                                                                                                                                 5G1.1 VL + KLV56 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                        (first
                                94US-0236208
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                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 323.8;
Pred. No. 3.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A DNA construct (AAT08485) codes for a humanised CDR-grafted and framework sequence-altered light chain, 5G1.1 VL + KLV56 (AAR77612), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (AAT0843) coding for a humanised Fd (AAR77610) into vector APEX-3P (AAT08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
Key
                         Homo sapiens
                                       Streptomyces avidinii
                                                                                                                                                                                                 AAC86562 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                   Synthetic
                                                                                          Streptavidin;
                                                                                                                   DNA encoding
                                                                                                                                              02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glomerulonephritis.
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                                                                           hematological
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGAACCTGGCAGATGGAGTGC 181
                                                                                                                                                                                                                                                                                                                                                                                                CTTCTCGCTTCTCGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCCGATATCCAGATGACCCAGTCCCCGTCCCTGTCCGCCTCTGTGGGCGATAGGG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTA 121
                                                                                                                                                                                                                                                              gacagggtaccaaggtggaaataaaacgaactgtggctgcaccatctg
                                                                                                                                                                                                                                                                                                                   aacctgaggacttcgctacgtattactgtcagaacgttttaaatactccgttgactttcg
                                                                                                                                                                                                                                                                                                                                             AGCCTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCG 301
                                                                                                                                                                                                                                                                                                                                                                      cttctcgcttctctggatccggctccggaaccgattacactctgaccatcagcagtctgc
                                                                                                                                                                                                                                                                                                                                                                                                                       aacctgggaaagctccgaagcttctgatttacggtgcgacgaacctggcagatggagtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcaccatcacctgcggcgccagcgaaaacatctatggcgcgctgaactggtatcaacgta 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgcaggatatccagatgacccagtccccgtcctctctgtccgcctctgtgggcgataggg 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MJ, Matis L, Mueller r RP, Springhorn J P, Y, Wilkins JA;
                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                   a
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                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to inhibit complement induced cell lysis
                                                                             malignancy;
                                                                                          tumour cell;
                                                                                                                 fusion of single chain antibody/streptavidin.
 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176
                                                                                                                                                                                                   DNA; 1612
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                                                                              huNR-LU-10;
                                                                                          cancer; adenocarcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 322.4;
Pred. No. 9.2e
0; Mismatches
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nto SP,
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                                                                              EGP40; EPCAM;
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Best Local:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour ce associated with cancer, e.g. adenocarcinomas or hematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer, e.g. adenocarcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-091213/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1612 BP; 353 A; 493 C; 459 G; 307 T; 0 other;
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                                                                                       CCTTCTCGCCTTCTCGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTG
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cagcctgaagatttcgcaacgtattactgtctacagcgtaatgcgtatccgtacacgttc
                                                                    ccatcaaggttcagtggcagtcgggtcagattatactctcaccatcagcagcctt 610
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                                                                                                                                                              AAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGAACCTGGCAGATGGAAGGC 180
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Example; Fig 5; 54pp; English
                                                                     WPI; 1992-024365/03.
P-PSDB; AAR20185.
                                                                                                                                                                                                                                                                                                                                        Sequence encoding the shortened hinge version of the \ensuremath{\text{B72.3}} single chain Fv hinge.
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                                 New multivalent antigen-binding proteins – comprise Fv fragment linked to at least 1 other Fv fragment spacer and useful for
                                                                                                     King DJ,
                                                                                                                                                    11-JUN-1990;
                                                                                                                                                                            11-JUN-1991;
                                                                                                                                                                                                                         WO9119739-A.
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                   Fv fragment;
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Matches
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21-AUG-2000
                             AAA15019
                                                         AAA15019 standard; DNA; 1925
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439; Conservative
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                                                                                                                                   treating a CD20+ malignancy acute or chronic leukemia,
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                                                                                                                    Example
                                                                                                                                          Genetically engineered CD20-specific redirected T cells useful treating a CD20+ malignancy, such as non-Hodykin's lymphoma or
                                                                                                                                                                                          Raubitschek A,
                                                                                                                                                                                                        (CITY ) CITY
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                                                                                                                                                                                                                                                                                                                                                      CD20-specific receptor; CD-20 speciifc redirected T cell; leukemia; CD20+ malignancy; non-Hodgkin's lymphoma; myeoablative chemotherapy;
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                                                                                                                                                                           2000-339676/29
                                                                                                                                                                                                                                                                                                                                              malignancy;
cell rescue;
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receptor comprising an intracellular signalling domain, a transmembrane domain and an extracellular domain, the extracellular domain comprising a CD20-specific receptor. The genetically engineered CD20-specific redirected T cells are useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a human patient having previously undergone myeoablative chemotherapy and stem cell rescue. The genetically engineered CD20-specific redirected T cells are also useful for abrogating an untoward B cell function, such The present sequence encodes a synthetic CD20-specific chimeric receptor. The specification describes CD-20 specific redirected T cells which express and bear on the cell surface membrane a CD20-chimeric as autoimmune disease (lupus or rheumatoid arthritis) in BP; 471 541 G; 359 ; 0 other; മ patient.

Sequence 1925 ? 554 C;

Query Match Best Local

Similarity

38.9%;

Score 290.6; DB 2 Pred. No. 9.6e-72;

DB 21;

Length

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                                                                                                                                                                                                                                       gacattgtgctgacccaatctccagctatcctgtctgcatctccaggggagaaggtcaca 146
                                                                                                                                                                                                                                                                      GATATCCAGATGACCCAGTCCCGTCCTCCCTGTCCGCCTCTGTGGGCGATAGGGTCACC
                                               cgcttcagtggcagtgggtctgggacctcttactctctcacaatcagcagagtggaggct
                                                                               CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT
                                                                                                            ggatcctcccccaaaccctggatttatgccacatccaacctggcttctggagtccctgct
                                                                                                                                           GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT
                                                                                                                                                                                                         ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
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RRSULT 1

AAZ88358

ID AAZ88

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DT 04-M

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                                                New o'ligonucleotide, autoimmune disease, infections diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bispecific anti-zeta-chain/anti-EpCAM antibody nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ88358 standard;
     Example 9;
                                                                                                                                                                                                                                            Reiter
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     Page 74;
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79pp;
                                                                            immune
                                                                              polypeptide, antibody useful for treating immune deficiencies, T-cell malignancies and
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  English
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cc least one complementary determining region (CDR) of a variable region of can antibody which specifically interacts with the extracellular domain of ct the human zeta-chain. The antibody whose CDR of a variable region is cc encoded by (I), is obtained by immunising a rat with jurkat cells and cc peptide having 11 N-terminal amino acids of a rat zeta-chain. The antibody is useful for the treatment and prevention of canti-zeta-chain antibody is useful for the treatment and prevention of cc infectious diseases, immune deficiencies, T-cell malignancies, in corder to avoid graft rejection after organ transplantation, malignancies, cc or viral infections. The antibody, and fragments of it, can be useful for the enhancement or suppression of NK-cell dependent immunity or for the ct treatment of NK-cell derived malignancies. It can also be useful for the cc treatment of zeta-chain or eta-chain expression on NK-cells, cc T-lymphocytes or their precursors. The present sequence encodes a construction of the constant or the constant sequence encodes a constant of the constant constant invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a nucleic acid molecule (I)
                                                   present
                                                      invention.
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Sequence 1637 BP; 398 A; 404 C; 436 ç; 399 Τ, 0 other;

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GCGCGCGTTATTTTTTGGTTCTAGCCCGAAT---TGGTATTTTGATGTTTTGGGGTCAAG
                                                                                                                                                                                                                               CCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGATTCAAT
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                                                                     CTAGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATT
                                                                                                 GTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGA
                                                                                                                                                         ggataaaacagcagcctggaaatggccttgagtggattgggtggatttatcctggaaatg
                                                                                                                                                                                       GGGTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTG
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                                          ccagcacagcctatatgcagctcagcagcctgacatctgaggactctgcagtctatttct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 290.4;
Pred. No. 1e-7
0; Mismatches
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Best L
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                                                                                                                                                                                                                                                                                                  assembled consisted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type I ribosome-inactivating protein; ricin; gelonin; immunoconjugate; autoimmune disease; cell killing; toxin; overlap extension polymerase chain reaction; H65 variable RMA; rabbit muscle aldolase; cathepsin cleavage; SLT; E.coli Shiga-like toxin; human engineered antibody; s
                                                                                                                                                                                                                                  consisted of the entire v and J region of one chain (heavy or light) linked to the entire v and J segment of the other (light or heavy) via a 15 amino acid flexible peptide. The scab was assembled in two orientations (see AAQ42284 and AAQ42285). A fusion construct prepared in which the natural sequence gelonin gene was positioned at the N-terminus and the SLT or RMA linker peptide was positioned
                                                                                                                                                                                                                                                                                                                                                                      Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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19-JUN-1992;
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Local Similarity
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GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT
                                                                                               GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGATAGGGTCACC
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                                    atcacttgccgggcgagtcaggacattaatagctatttaagctggttccagcagaaacca
                                                 ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
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                                                                                  gacatccagatgactcagtctccatcttccctgtctgcatctgtaggagacagagtcact
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                                                                                                                                                                                                                                                                                                            chain antibody form of the he3 H65 variable domain was from previously constructed genes. This scAb segment
                                                                                                                                    Conservative
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92US-0901707.
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                        25-JAN-1999;
07-OCT-1999;
                                                  15-JAN-1999;
                                                                           13-JAN-2000; 2000WO-EP00245.
                                                                                                      20-JUL-2000.
                                                                                                                               WO200041474-A2.
                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                             pone
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host versus graft disease; graft versus
                                                                                                                                                                                                                                                  Immunotoxin;
                                                                                                                                                                                                                                                                          DNA encoding
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                                                                                                                                                          aeruginosa
                                                                                                                                                                                                           transplant; ss
                                                                                                                                                                                                                                                  CD3-binding domain; Pseudomonas exotoxin A; immune system;
                                                                                                                                                                                                                                                                          an immunotoxin comprising a CD3
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                        99US-0232445.
99US-0236968.
99US-0414134.
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Best Local Similarity
Matches 454; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant immunotoxin used for prophylaxis and treatment of T-cell mediated diseases e.g. transplantation rejection -
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tacaa;eggtgttagtacctacaaccagaagttcaaggacaaggccacattaactgtagac
                                    GGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGAC 597
                                                                                               CCAGGGGCCTCAGTCAAAGTGTCCCTGTAAAGCTAGCGGCTATATTTTTTTCTAATTAGTTGG
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                                                                         atgaactgggtgaagcagagtcatggaaagaaccttgagtggatgggacttattaatcct
                                                                                                                                                   cctggagcttcaatgaagatatcctgcaaggcttctggttactcattcactggctacacc 480
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Pred. No. 8e-66;
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                                                                                                        aagtcatccagcacagcctacatggaactcctcagtctgacatctgaggactctgcagtc
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Search completed: July 20, Job time: 4412 sec 2001, 02:38:19

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Match
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
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US-08-839-765-89
US-09-136-389-89
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US-08-926-789-15
US-08-926-789-15
US-08-926-789-15
US-08-923-854-24
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US-07-988-430-92
US-08-425-336-89
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                  46, Appl
42, Appl
3, Appli
3, Appli
29, Appl
17, Appl
18, Appl
19, Appl
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220.6	220.6	221.8	223.2	223.2	224.4	224.4	227.6	227.6	227.6	230.6	230.6	230.6	230.6	230.6	230.6	231	231
29.5	29.5	29.7	29.9	29.9	30.0	30.0	30.5	30.5	30.5	30.9	30.9	30.9	30.9	30.9	30.9	30.9	30.9
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## ALIGNMENTS

RESULT 1 US-08-400-115-3

Sequence 3 Patent No.

3, Application US/08400115 5. 5864019

GENERAL INFORMATION:
APPLICANT: KING, David
APPLICANT: MOUNTAIN, An
APPLICANT: OWENS, Raymo
APPLICANT: YARRANTON, G

KING, David John MOUNTAIN, Andrew OWENS, Raymond John YARRANTON, Geoffrey Thomas

```
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,115
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,136
FILING DATE: 27-SEP-1993
PRIOR APPLICATION NUMBER: US 07/842,193
PRIOR APPLICATION NUMBER: US 07/842,193
FILING DATE: 17-MAR-1992
                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                               FILING DATE: 11-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 040283/0106 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/GB91/00935
FILING DATE: 11-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9012995.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Multivalent Antigen-Binding Proteins NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                              TELLERAX: (20-
TELEFAX: 904136
TYPE: nucleion STRANDEDNESS:
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T: 3000 K Street, N.W.,
Washington, D.C.
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Best Local S
Matches 439
                                                                                          Sequence 92, Application Patent No. 5416202 GENERAL INFORMATION:
                                                                                                                   Sequence 92,
        APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Co
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FEATURE:
NAME/KEY:
LOCATION:
NUMBER OF SEQUENCES:
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Preparation 101
        Materials Comprising and Methods of Preparation and Use for Ribosome-In
                                                                                                                    US/07988430
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Pred. No. 6.2e-84;
0; Mismatches 220
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         Ribosome-Inactivating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION UNMER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5416202and, Greta E.
PROTECTOR OF TOWN NUMBER: US 0302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two First
STREET: Street
CITY: Chicago
STATE: Illinois
355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35: REFERENCE/DOCKET NUMBER:
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                                                           GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
                                                                                                                                                                                                                                                                        GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGAACCTGGCAGATGGAGTCCCTTCT 186
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             GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCC
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GGTGGAGGATCTGAGATCCAGTTGGTGCAGTCTGGAGGAGGCCTGGTGAAGCCTGGAGGG
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63.7%;
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           TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
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Patent No. 5621083
GENERAL INFORMATION:
                                                                                                                                                    APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
APPLICATION NUMBER: US 07/787,567
APPLICATION NUMBER: US 07/787,567
APPLICATION NUMBER: 05/089
APPLICATION NUMBER: P-36,989
RECISTRATION NUMBER: P-36,989
RECISTRATION NUMBER: P-36,989
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
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                                                                     TELEPHONE: 312/474-0448
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CITY: Chicago
                                                                                                                                           REFERENCE/DOCKET NUMBER:
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South Wacker Drive
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: 1
US-08-425-336-89
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US-08-488-113B-89
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                                                          Sequence 89, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
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Best Local 9
APPLICANT: Carroll, APPLICANT: Studnika, TITLE OF INVENTION: TITLE OF INVENTION:
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                             Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
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 Proteins
                Immunotoxins Comprising Ribosome-Inactivating
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Pred. No. 1.4e-80;
0; Mismatches 251;
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Best Local Similarity
Matches 472; Conserv
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
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LENGTH: 723 base pairs
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PRIOR APPLICATION DATA:
US 08/425,336
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/488,113B FILING DATE: 07-JUN-1995
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                   GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                  AGGTTCAGTGGCAGTGGATCTGGGACAGATTATACTCTCACCATCAGCAGCCTGCAATAT
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GAAGATTTTGGAATTTATTGTCAACAGTATGATGAGTCTCCGTGGACGTTCGGTGGA 300
                                                                                                     CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.4e-80;
0; Mismatches 251;
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US-08-477-484B-89; Sequence 89, Application US/08477484B; Patent No. 5756699
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                                                               FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: US 08/064,691
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Immunoto:
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                                  PRIOR APPLICATION DATA:
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500 West Madison Street, 34t
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MBER: US 07/901,707
19-JUN-1992
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-889
TELEPAX: 312/707-9155
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LENGTH: 723 base pairs
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
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 ACAAGACGGGGTTACG---
                                                                                                                         GAGCCAACATATGCTGATTCTTTCAAGGGACGGTTTACCTTCTCTTTGGACGATTCTAAG
                                                                                                                                                                                       GAAGATTTTGGAATTTATTATTGTCAACAGTATGATGAGTCTCCGTGGACGTTCGGTGGA 300
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                              GCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACC 726
                                                             ACACTGCCTATTTACAGATCAACAGCCTCAGAGCCGAGGACACGGCTGTGTATTTCTGT
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                                                                                                                                                                                                                      GTGCGTCAGGCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGT 546
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                                                                                            AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC
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Pred. No. 1.4
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- ACTGGTACTTCGATGTCTGGGGCCAAGGGACC
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RESULT 6
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                                 Query Match
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Proteins
TYPE OF THE TRANSPORTER OF T
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APPLICANT: Carroll, Stephen |
APPLICANT: Studnika, Gary M.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-JUN-1992 PRIOR APPLICATION DATA:
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TOPOLOGY: lir
                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/901,707
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 37.9%;
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Conservative
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 ; Score 283.4;
; Pred. No. 1.4e
0; Mismatches
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RESULT 7
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Patent No. 6146631
GENERAL INFORMATION:
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APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 472; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO:
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FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
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FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPAX: 312/707-9155
TELEPAX: 312/707-9155
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LENGTH: 723 base pairs
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GTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGT
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                               TCCGTCAGAATCTCCTGCGCAGCTTCTGGGTATACCTTCACAAACTATGGAATGAACTGG
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09-DEC-1992
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Pred. No. 1.4e-80;
0; Mismatches 251;
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US-09-136-389-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/646
FILING DATE: 13-MAY 1996
APPLICATION NUMBER: PCT/US
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
 INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                              APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-WAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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                                            TELEPHONE: 312/707-8889
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                                                                       NAME: MCNicholas, Janet M. REGISTRATION NUMBER: 32,918 REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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Studnika, Gary M.
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RESULT 9
PCT-US92-09487-92
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Best Local Similarity 63.7%;
Matches 472; Conservative
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                                                             ACGGTCACCGTCTCCTCATGA 723
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Pred. No. 1.4e-E
0; Mismatches
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Sequence 92, Application PC/TUS9209487 GENERAL INFORMATION:

APPLICANT:
APPLICANT:

Bernhard, Susan L. Better, Marc D. Carroll, Stephen F

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NOLand, Greta E.
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/901,707
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19921104
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                           7 GATATCCAGATGACCCAGTCCCCGTCCTCCTCTCCGCCTCTGTGGGCGGATAGGGTCACC 66
GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                              CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCAGTCT 246
                                                                                                                                                                                              GGGAAAGCTCCTAAGACCCTGATCTATCGTGCAAACAGATTGGAATCTGGGGGTCCCATCA 180
                                                                                                                                                                                                                      GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
                                                                                                                                                                                                                                                                    ATCACTTGCCGGGCGAGTCAGGACATTAATAGCTATTTAAGCTGGTTCCAGCAGAAACCA 120
                                                     GAAGATTTTGGAATTTATTGTCAACAGTATGATGAGTCTCCGTGGACGTTCGGTGGA 300
                                                                                                                                                                                                                                                                                            ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                                                                                                                                                                                                                                                                                             GACATCCAGATGACTCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGAGACAGAGTCACT 60
                                                                                                                          AGGTTCAGTGGCAGTGGATCTGGGACAGATTATACTCTCACCATCAGCAGCCTGCAATAT 240
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 283.4; DB 5;
Pred. No. 1.4e-80;
0; Mismatches 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4
                                                                  FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 1
APPLICANT: 1
                                                                                                                                                                                  APPLICATION NUMBER: WO PFILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 6
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
                                                     TELEPHONE:
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Boque, Lluis
Wlodawo
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RESULT 11
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; LOCATION: 1..1065
; OTHER INFORMATION:
US-08-875-811-40
GENERAL INFORMATION:
APPLICANT: Rybak,
APPLICANT: Newton,
APPLICANT: Boque,
                                                 Sequence 48, Application Patent No. 6045793
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STRANDEDNESS: single
TOPOLOGY: linear
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 Boque, Lluis
            Rybak, Susanna
Newton, Dianne
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                                                              US/08875811
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMEER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION OBTA:
APPLICATION OBTA:
APPLICATION UNMEER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAT1S, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-2441000
FELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0300
FELEERAY: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SECHIEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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LENGTH: 1065 base pairs
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CORRESPONDENCE ADDRESS
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301
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%;
Local Similarity 63.4%;
es 427; Conservation
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LOCATION: 1..1065
OTHER INFORMATION:
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01 FILING DATE: 19-FEB-1998
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                                                                                                                                                                                                                            GGGAAATCTCCTAAGACCCTGATCTATCGTGCAAACAGACTGGTAGATGGGGGTCCCATCA 180
                                                                                                                                                                                                                                                                                                    TTCACTTGCAAGGCGAGTCAGGACATTAATAACTATTTATGCTGGTTCCAGCAGAAACCA 120
                 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGGTGGATCTGGT 366
                                                                          GAAGATATGGGAATTTATTATTGTCTACAGTATGATGAGTTTCCGTACACGTTCGGAGGG
                                                                                                         GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                     CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
                                                                                                                                                                                                                                                             GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
                                                                                                                                                                                                                                                                                                                        ATCACCTGCGGCGCCAGACAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
GGGACCAAGCTGGAAATAAAA - - - - -
                                                                                                                                                  AGGTTCAGTGGCAGTGGATCTGGACAAGATTATTCTCTCACCATTAGCAGCCTGGAGTAT 240
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Two Embarcadero Center, Eighth Floor
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-GGAGGCGGTGGCTCGGGCGGTGGCGGATCGGGT
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US-08-875-811-44
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GENERAL INFORMATION:
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                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19 FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
APPLICATION NUMBER: US 60/011,800
APPLICATION NUMBER: US 60/011,800
APPLICATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
                                                                                  TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE:
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                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/875,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                      576-0300
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; NAME/KEY: CDS
; LOCATION: 1..1074
; OTHER INFORMATION:
US-08-875-811-44
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                                                                                                                          Sequence 50, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
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                                            APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease
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             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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ADDRESSEE:
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                                                                                                                                                                                                                                                                             GCGCGTTATTTTT 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGAAATCTCCTAAGACCCTGATCTATCGTGCAAACAGACTGGTAGATGGGGTCCCATCA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGAACTGGTATCAACGTAAACCT 126
                                                                                                                                                                                                                                                ACCCCTCTTTATT 1021
                                                                                                                                                                                                                                                                                                                                               AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC
                                                                                                                                                                                                                                                                                                                                                                               AGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGT
                                                                                                                                                                                                                                                                                                             AGCACTGCCTACATGGAACTCAACAGCCTGACAAATGAGGACTCTGCGGGTCTATTACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAAACAGAGGCCTGGACAGGGTCTGGACTGGATTGTCGCTATTGATCCTCGAAATAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427;
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Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.7%;
63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "MetSerOncA87FBE6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 267; DB 3; Pred. No. 2.7e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240;
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; LOCATION: 1..1074
; OTHER INFORMATION:
US-08-875-811-50
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FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REFERENCE/DOCKET NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
TYPE: 1074 base pairs
TYPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.7%; Score 267; DB 3; Best Local Similarity 63.4%; Pred. No. 2.7e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 427; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CITY: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GATATCCAGATGACCCAGTCCCCGTCCTCTGTGCGCCTCTGTGGGGCGATAGGGTCACC
                                                                                                                                                                         GAAGATATGGGAATTTATTATTGTCTACAGTATGATGAGTTTCCGTACACGTTCGGAGGG
                                                                                                                                                                                                                                                             AGGTTCAGTGGCAGTGGATCTGGACAAGATTATTCTCTCACCATTAGCAGCCTGGAGTAT
                                                                                                                                                                                                                                                                                                     CGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
                                                                                                                                                                                                                                                                                                                                                                      GGGAAAGCTCCGAAGCTTCTGATTTACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCT 186
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                        GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCC 426
                                                                                                                              GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGGTGGATCTGGT 366
                                                                                                                                                                                                                 GAAGACTTCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
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San Francisco
California
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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19-FEB-1998
ON: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 240; Indels
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; NAME/KEY: CDS
; LOCATION: 1..1083
; OTHER INFORMATION:
US-08-875-811-46
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                                                                                                                                                                                               TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Newton, Dianne -- APPLICANT: Newton, Dianne -- APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
APPLICANT: Wlodawer, Recombinant Ribonuclease Proteins
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                        FEATURE:
                                                                                     MOLECULE TYPE:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1086 base pairs
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                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      STRANDEDNESS: single
                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAAACAGAGGCCTGGACAGGGTCTGGACTGGATTGTCGCTATTGATCCTCGAAATAGT 888
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                                                                                                                                                                                                                  (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                         linear
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              /note= "MetSerOncAngsFv"
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RESULT 15
US-08-875-811-42
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                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                        1015
                                                                                                                                     APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                    607
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CITY: San Francisco
STATE: California
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              COUNTRY:
                                                                            ADDRESSEE:
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Similarity 63.4%;
94111-3834
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: si
TOPOLOGY: linear
MOLECULE TYPE: DNA
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LENGTH: 1137 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                  TCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTTCCAGCTACTGGATGCACTGG
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		080	566	1020	506	960

Search completed: July 20, 2001, 02:35:04 Job time: 6177 sec

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Search information block:
Query: US-08-487-283A-8
Query length: 747
Database: PIR 68:*
Database sequences: 219241
Database length: 76174552
        pir2:S40349
pir2:S29257
pir2:S36269
pir2:C33548
pir2:C33548
pir1:K1HULY
pir2:S47182
pir2:S47182
                                                                                    pir2:PH0961
pir2:S44122
pir2:S19665
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-QB=-PIR_68 -QFMT=fastan -SUFFIX+tra.rpr -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-QGAPOP4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YTART=1 -MATRIX=Dlosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM-ext -MINLEN=0 -MAXLEN=200000000
-USER-US08487283_@CGN1_1_126 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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pir2:A33548
pir2:JL0139
pir2:S24217
pir2:S34014
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A; Molecule type: DNA
A; Residues: 1-287 <SUZ>
C; Keywords: fusion protein
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R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune,
J. Biochem. 122, 322-329, 1997
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pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion
C:Species: synthetic
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
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A; Reference number: PC4402
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hrGlyAlaGlnThrGluAspGluAlaIleTyrPheCysAlaLeuTrpTyr 119
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A; Molecule type: mRNA
A; Residues: 1-142 <LAR>
A; Cross-references: GB:M26463
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: himmunoglobulin homology <IMM>
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Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C Blochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi A;Reference number: A32483; MUID:89273586
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Ratio:
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C;Accession: $40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and A;Reference number: $40312; MUID:94080891
A;Accession: $40367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V-J-C region - human
C; Species: Homo sapiens (man)
C; Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-127 <KLE>
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                                                                                                                                                                                                                                                                     AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe
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                                                                                          laThrTyrTyrCysGlnGlnSerTyrAsnThrProTrpThrPheGlyGln
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Ratio:
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4.716
93.578
                                                                                                                                                                                                                                                                                             Length: 109
Gaps: 0
Percent Identity: 86.239
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                                                                                                                                    306
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seq_documentation_block:
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S36265
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, JEMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36265
                                                         seq_documentation_block:
If heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, J. Mol. Biol. 239, 68-78, 1994 A;Title: In vitro assembly of reper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-487-283A-8 x S36265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
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                                                                                                                                                                         seq_name: pir2:S46393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-118 <GRI>
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                                                                                                                                                                                                                 uValThrValSerSer 118
                                                                                                                                                                                                                                                     GGTCACTGTCTCGAGC 744
                                                                                                                                                                                                                                                                                                                                                                     erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgAspPhe
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4.250
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                                     G.; Griffiths,
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 on
the surface of phage by
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-129 <FIC>
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                    A;Title: Amino acid substitutions in V-H CDR2 change the A;Reference number: A30562; MUID:89110066 A;Accession: C30562
                                                                                                                                                                                                                                           seq_documentation_block:
Ig heavy Chain V region (27.7.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989
C;Accession: C30562
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Quality:
                                                                  A; Molecule type: mRNA
A; Residues: 1-119 <SIK>
                                                                                                                                                                                                    R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, J. Immunol. 142, 888-893, 1989
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US-08-487-283A-8 x
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                                                                                                           A; Status: preliminary
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86.822
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6
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A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                              alignment_block:
US-08-487-283A-8 x B49047
                                                                                                                                                                                                                                                                                                                                   Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224
A;Accession: B49047
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human C:Species: Homo sapiens (man) C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
    Quality:
                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                               A; Molecule type: nucleic acid
A; Residues: 1-108 <VIC>
                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:B49047
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                                                                                          Percent Similarity:
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Align seg ·1/1
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TyrGlySerSer..........PheAlaTyrTrpGlyGlnGlyThrLe 114
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                                                                                                                             Quality:
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                                                                                                            Ratio:
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ţo:
B49047
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93.519
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from:
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-135 <MAH>
A;Cross references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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A; Accession: S49530
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US-08-487-283A-8 x S49530
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                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: S49530
                 517 TGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GlyThrLysValGluIleLysArg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                      417 GCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTT
                                                                                                                                                                                                                                                                                          367 GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                       467 CTAATTATTGGATTCAATGGGTGCGTCAGGCCCCGGGCAGGGCCTGGAA
                                                                            49 hrGlyTyrTyrMetHisTrpValArgGlnAlaProGlyGlnGlyLeuGlu
                                                                                                                                                                84 laThrTyrTyrCysGlnGlnSerTyrSerThrProLeuThrPheGlyGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
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66 TrpMetGlyTrpIleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLy
                                                                                                                                                                                                                                               16 GlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGluValLysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>بــ</u>
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4.266
86.508
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Ig heavy chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Accession: E30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
J. Immunol. 142, 888-893, 1999
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi A;Reference number: A30562; MUID:89110066
A;Accession: E30562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-119 <SIK>
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                                                                                                                                                                                                                                               ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTTAAAGACCG
                                                                                                                                                                                                                                                                                                                                                                                      AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC 666
                    TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT
                                                        erSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgHisTyr
                                                                                                   sAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeuS
                                                                                                                                                                                                                                                                                                       leGluTrpValLysGlnArgProGlyHisGlyLeuGluTrpIleGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrMetGluLeuSerArgLeuArgSerAspAspThrAlaValTyrTyrCys 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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4.261
89.344
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69
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C; Accession: S23623
R; Olee, T.; Lu, E.W
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seq_documentation_block:
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;32-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi
A;Reference number: S40312; MUID:94080891
A;Accession: S40331
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Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar_1994 #sequence_revision 26-May-1995 #text_change
                                                                                                            seq_name: pir2:S23623
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US-08-487-283A-8
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A; Residues: 1-123 <KLE>
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Percent Similarity:
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||||||||||||||:::
uValThrValSerAla 119
                                                                                                                                                                                   GGTACCAAGGTGGAAATAAAA 327
                                                                                                                                                                                                                                                                       CTACGTATTACTGTCAGAACGTTTTAAATACTCCGGTTGACTTTCGGACAG
                                                                                                                                                                                                                                                                                                                                                             CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGACGAACCTGGCAGATGGAGTCCCCTTCTCGCTTCTCTGGATCCGGCTC
                                                                                                                                                          GlyThrLysValGluIleLys 123
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4.620
93.458
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Percent Identity:
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T.; Lu, E.W.; Huang, D.F.; Soto-Gil,

R.W.; Deftos, M.;

Kozin,

F.; Carson,

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seq_documentation_block:
Ig heavy chain V region (27.4b.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23:Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: D30562
R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A:Reference number: A30562; MUID:89110066
A:Accession: D30562
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IVM>
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                                                                             A; Molecule type: mRNA
A; Residues: 1-119 <SIK>
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US-08-487-283A-8 x S23623
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A; Residues: 1-171 <OLE>
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A;Accession: S23623
A;Status: preliminary
                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: pir2:D30562
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A; Title: Genetic analysis of se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: S23623 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 TTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTAT 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 TGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAA 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 GCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAATTATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCAGGGCCTGGAA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaIleGluTyrPheTyrAspGlySerAspLeuLysProSerAspValPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TrpMetGlyTrpIleAsnProAsnSerGlyGlyThrGlyTyrGlyGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eAspIleTrpGlyGlnGlyThrMetValThrValSerSer 145
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4.153
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Percent Identity: 70.769
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A;Status: preliminary; nucleic acid sequence not shown; not com A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-123 <KIP> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable reginal R;Reference number: A33548; MUID: 89345575
A;Accession: D33548
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Quality:
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                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: pir2:D33548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to:
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 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                heavy chain V-1 region (WIL2) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   729 GGTCACTGTCTCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 TyrGlySerSerSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            679 TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 IlePheProGlySerGlySerSerAsnTyrSerGluLysPheLysGlyLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 rValLysIleSerCysLysAlaThrGlyTyrThrPheSerSerTyrTrpI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 sAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeuS
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                   Ratio:
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458.50
4.168
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Percent Identity: 72.358
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|PheAlaTyrTrpGlyGlnGlyThrLe
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Gaps:
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alignment\_block: US-08-487-283A-8 x D33548

Align seg

1/1

to:

D33548

from:

1 to:

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A; Molecule type: mRNA
A; Residues: 1-114 <SHE>
A; Residues: 1-114 <SHE>
A; Residues: 1-114 <SHE>
C; Comment: This protein is an anti-double-stranded DNA antibody.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 20-94/Domain: immunoglobulin homology <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A novel class of anti-DNA antibodies identified in BALB/c mice. A;Reference number: PT0352; MUID:91108325
A;Accession: PT0358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region (7D2.G12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C;Accession: PT0358
                                                                                                                                                                                                                                                                                    alignment_block:
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                                                                TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAAC 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGGTATCAACCTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGGTCACTGTCTCGAGC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrCysGlyTyrAspCysTyrTyrPhePheAspTyrTrpGlyGlnGlyTh 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gValThrIleThrArgAspThrSerIleAsnThrAlaTyrMetGluLeuS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rLeuValThrValSerSer 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArgAlaSer 100
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                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                      457.00
4.570
92.593
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                                                                                                                                                                                                                                                                                                                          80.556
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R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
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F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;36-50/Region:
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                                                                                                                                                                                                                                                                                                                                                                           US-08-487-283A-8 x PH0954
                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                 579
                                                                                                     529
                                                                                                                                                                       479
                                                                                                                                                                                                                                          429
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               TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
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                                                                                                   ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                      AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTTCTAATTATTGGA 478
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gValThrIleThrAlaAspGluSerThrSerThrAlaTyrMetGluLeuS
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4.183
82.576
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117 rGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 132
706GATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC 744
101 AlaSerIleAspAspPheTrpSerGlyTyrTyrProAsnTyrTyrTyrTy 117
629 CCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCGCGT 672

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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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-DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
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-TRANS-human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-THR_MAX-100 -THR_MIN-0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -MINLEN-0 -MAXLEN-200000000
-USER-US09487283_@CGN1_1_56 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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AC P01600;
DT 21-JUL-1986 (Rel. 01,
DT 21-JUL-1999 (Rel. 38,
DE IG KAPPA CHAIN V-I RE
OS HOMO Saplens (Human).
OC Eukaryota; Metazoa; C
OC Mammalla; Butheria; P
OX NCBI_TaxID=9606;
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RN [2]
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RN MEDLINE=71032830; Pub
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CR PIR; A01868; KIHUHUI.
DR INTEPPO; IPR003006;
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SwissProt_39:KV3L_HUMAN +
SwissProt_39:HV38_MOUSE +
SwissProt_39:KV5J_MOUSE +
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"The primary structure of a monoclonal kappa-type immunoglobulin chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups.";
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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FRAMEWORK 1.
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08D3A6160D8D0618 CRC64;
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3.2e-24
5.1e-24
5.2e-24
6.2e-24
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P18135
P01613
P01808
P01643
                                                                                                                                                                                                                          (3) MARKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 homo sapiens
5 homo sapiens
3 homo sapiens
8 mus musculus
3 mus musculus
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alignment_block:
US-08-487-283A-8 x KV1M_HUMAN
                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: SwissProt_39:KV1M_HUMAN
                                                                                                                         Align seg 1/1 to: KV1M_HUMAN
                                                                                                                                                                                       Percent Similarity:
                                             . 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
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DOMAIN
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                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01871; K1HULY.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete amino acid sequence of the variable domains of IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capra J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=77038198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KV1M_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDICEPTION OF THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAPPA CHAIN V-I REGION LAY.
ACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
                                               TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGA 106
                                                                                              GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGA
                       pArgValThrIleThrCysGlnAlaSerGlnAsnValAsnAlaTyrLeuA
                                                                        GlyThrArgValGluIleLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTACCAAGGTGGAAATAAAACGT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laThrTyrTyrCysGlnGlnAsnTyrIleThrProThrSerPheGlyGln 100
                                                                                                                                                                                                     Ratio:
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                                                                                                                                                                                                                                                                                          7 region.
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4.557
89.815
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                FRAMEWORK 3
                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK 1
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                                                                                                                                                                                                                                                                  739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                          SIMILARITY.
                                                                                                                                                                                       Identity:
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                                                                                                                                                                                                                 Length:
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alignment_block:
US-08-487-283A-8
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                                                            Align seg
                                                                                                                                        Percent Similarity:
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                367 GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAA 416
                                                                                                                                                                                                                                                                            InterPro; interPro; 1; 1; 1. Pfam; PF00047; ig; 1. Immunoglobulin V region; 1
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-RROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Evolutionary aspects of immunoglobulin heavy con gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01743;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                           PIR; A02024; HVHUHG.
                                                                                                                                                                                                                                                                                                                                                         EMBL; J00240; AAA52988.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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16 GlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGluValLysLy
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                                                                                                                                                                                                                                   117 AA;
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                                                            HV1B_HUMAN
                                                                                           HV1B_HUMAN
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                                                                                                                                      437.00
4.505
95.098
                                                                                                                                                                                                                                   12946 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                            Signal.
                                                                                                                                Length: 102
Gaps: 0
Percent Identity: 82.353
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                                                                                                                                                                                                                                   2D3F92FC60CD1FE7 CRC64;
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seq_name: SwissProt_39:HV07_MOUSE
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                                                                                                                            InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region
                                                                                                                                                                 PIR;
                                                                                                                                                                           EMBL;
                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                               "Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
Mus musculus (Mouse).
Eukarrota. Val-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
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                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                          Bothwell A.L.M., Paskind
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCGT 672
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                                                                                                                                                                A02034; MHMS18
                                                                                                                                                                                                                                                                                                      (NPB ANTIBODIES).
                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
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region;
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Rodentia;
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D SEGMENT.
JH2 SEGMEN
BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                     contribution evident in a
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                                    FRAMEWORK 3.
                                                  COMPLEMENTARITY - DETERMINING
                                                            COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                     IG HEAVY CHI
FRAMEWORK 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                  HEAVY CHAIN V REGION
              SEGMENT
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US-08-487-283A-8 x HV07_MOUSE
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                                                                                                                      Goni F., Frangione B.;

*Amino acid sequence of the Fv region of a human monoclonal IgM

(protein Wea) with antibody activity against 3,4-pyruvylated

galactose in Klabsiella polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-484[1983).

-I-MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

-AGAINST 3,4-PYRUYYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH

WALDENSTROM'S MACROGLOBULINEMIA.
                                       PIR; A01876; K1HUWE. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence upontation in the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV1R_HUMAN P01610;
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US-08-487-283A-8 x
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Shinoda T.;
"Comparative structural studies on the light chains of human "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
J. Bicchem. 77:1277-1296(1975).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARK
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                                                                                                                                             MEDLINE=76189985;
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION KA.
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P01603;
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Pfam; PF00047; ig; 1.
Immunoglobulin V region
                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-I REGION ROY.
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HSSP; P80362; 1WTL.
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PubMed=5595110

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seq_documentation_block:
ID KV1W_HUMAN STANN
AC P04431;
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US-08-487-283A-8 x KV1P_HUMAN
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                                                                                             seq_name: SwissProt_39:KV1W_HUMAN
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"Cum.).";
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(In) Franek F., Shugar D. (eds.);
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
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Klobeck H.G., Combriato G., Zacha
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla
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-I- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF TREGION OF THE KAPPA CHAIN REI.
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protein Au).";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sec
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"The structure determination of the variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=72189444; PubMed=5028201;
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
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COMPLEMENTARITY-DETERMINING
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KV10_HUMAN STANDARD;
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                                                                                                                                                                                               PIR;
PDB;
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1REI; 17-FEB-84.
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                                                  COMPLEMENTARITY - DETERMINING
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                             21-JUL-1986 (Rel. 01, Created)
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           307 GGTACCAAGGTGGAAATAAAACGT 330
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-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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COMPLEMENTARITY-DETERMINING
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ID KVIN_HUMAN STANDARD;
AC P01606;
AC P01606;
DT 21-JUL-1986 (Rel. 01, Creation of the control of the
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US-08-487-283A-8 x KV1N_HUMAN
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Science 169:56-59(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-I REGION OU.
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"Comparison of crystal structures of two homologous prostructural origin of altered domain interactions in imm light-chain dimers.";
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MEDLINE-81267384; PubMed-6167731;
Stevens F.J., Westholm F.A., Pana
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1995 (Rel. 32, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-I REGION WAT.
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MEDLINE=95086080; PubMed=7993911;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

MCBI_TaxID=9606;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION GAL.
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kappa-type, subgroup I.";
Hoppe-Seyler's Z. Physiol. Chem. 354:150
-i- MISCELLANEOUS: THE C REGION OF THIS
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    Physiol. Chem. 354:1503-1504(1973).
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-DB-SPTREMBL_16 -QFMT-fastan -SUFFIX-tra.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -MINLEN-0 -MAXLEN-2000000000
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sp_rodent:Q9JL80
sp_rodent:Q9JL78
sp_human:Q9UL73
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US-08-487-283A-8
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InterPro; IPR003596; -.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
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MEDLINE-98277139; PubMed-9614934;
Wan der Merwe P.L.,
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Clin. Immunol. Immunopathol. 87:18
-!- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Q9UL92;
Q9UL92;
Q9UH92;
Q9UH92;
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                           EMBL; AF035022; AAD56258.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7e-21
1.5e-20
2.2e-20
2.8e-20
7.5e-20
                                                                                                                                                                                                                                                                rheumatic
                                                                                                                                                                                                                                                                                            Kalis
                                                                                                                                                                                                                       MAJOR
                                                                                                                                                                                                                                                                                           N.N.,
                                                                                                                                                                                                                       HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
109
103
101
119
                                                                                                                                                                                                                                                                                            Berney
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Q9n0w5
Q9j180
Q9j178
Q9u173
                                                                                                                                                                                                                                                                                                                                                                                                            REGION (FRAGMENT).
                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 oryctolagus cuniculus
5 oryctolagus cuniculus
0 mus musculus (mouse).
8 mus musculus (mouse).
3 homo sapiens (human).
                                                                                                                                                                                                                                                                   normal
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SO TIPE DE COCRETE A REPRESENTATION DE COCRETA A REPRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-487-283A-8 x Q9UL94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q9UL94 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
N. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003596; -.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
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                                                                                                                                                                                                                                                                                                                                                            479
                                                                                                                                                                                                                                                                                                                                                                                                                                  429 AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTTCTAATTATTGGA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clin.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035020; AAD56256.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 TyrValValValProAlaAlaPheSerArgPheAspTyrTrpGlyGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus."
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                                                                                                                                    TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT 628
                                                                                                                                                                                                                                              ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                                                                                                                                 etHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTrp
                                                                                                                                                                                                                                                                                                                                                                                                         rValLysValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrTyrM 34
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Ratio:
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119 AA;
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4.142
89.344
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; 13205 MW; 13E64F5345F4A16E CRC64;
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Gaps: 1
Percent Identity: 71.311
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alignment_block:
US-08-487-283A-8 x Q9UL77
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Quality:
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                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TIEMBLIEL 13, Created)
01-MAY-2000 (TIEMBLIEL 13, Last sequence update)
01-MAR-2001 (TIEMBLIEL 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                      207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF035037; AAD56273.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus."
                                               51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin-reactive autoantibodies in rheumatic carditis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 ...GlyGlyGlyArgGlyLeuTrpPheAspProTrpGlyGlnGlyThrLe
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                                                                                                                                                                                           CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG
                                                          GCGACGAACCTGGCAGATGGAGTCCCCTTCTCGCTTCTCTGGATCCGGCTC
                                                                                                                                              TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN.
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rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA
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           Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunopathol. 87:184-19: TO IMMUNOGLOBULIN AND
                                                                                                                                                                                                                                            Q9UL77
                                                                                                                                                                                                                                                                                                        451.00
4.510
92.593
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                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                        Length: 108
Gaps: 0
Percent Identity: 81.481
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                                                                                                                                                                                                                                                                                                                                                                                  C06681716C4D16F3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                       156
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 84
                      256
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US-08-487-283A-8 x
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                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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Q9UL95 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q90L95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003596; -. Pfam; PF00047; 1g; 1. SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fetus.";
Clin. Immunol. Immunopathol. 87:18
-!- SIMILARITY: TO IMMUNOGLOBULIN
 629
                                                 579
                                                                                                   529
                                                                                                                                                     429
                                                                                                                                                                                                                                                        379 CAAGTCCAACTGGTGCAATCCGGCGCGCGAGGTCAAGAAGCCAGGGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035019; AAD56255.1; InterPro; IPR003006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
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                                                                          51
                        67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin-reactive autoantibodies in rheumatic carditis and
                                                                                                                                                                                                                             1 GluValGlnLeuValGluSerGlyAlaGluValLysLysProGlyAlaSe
                                      TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                                                                                                                                            DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laThrTyrTyrCysGlnGlnSerTyrSerThrSerTrpThrPheGlyGlu
gValThrMetThrArgAspThrThrIleSerThrAlaTyrMetGluLeuS
                                                                                                  ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                        etHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTrp
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                                                                          IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysValGlnGlyAr
                                                                                                                                                                                                                                                                                                                                                                       Quality:
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125 i
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4.096
87.200
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Gaps:
Percent Identity:
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BULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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alignment_block:
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                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                     US-08-487-283A-8 x Q9UL89
                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UL89 PRELIMINARY; PRT; 116 AA.
Q9UL89;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       591
                                                                     541 TCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGAC
                                                                                                                                                                    441 CTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGATTCAATGGGTGC 490
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; -. InterPro; IPR003596; -. Pfam; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HI
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                                                                                                                     491 GTCAGGCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF035025; AAD56261.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu X., Liu B.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GlyGlyGlyArgIleAlaAlaAlaGlyAspAlaPheAspIleTrpGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                               LeuGlyIleAlaAsnTyrAlaGlnLysPheGlnGlyArgValThrIleTh
                                                                                              DOMAIN.
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Quality:
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116 /
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4.320
87.288
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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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Q99YZ2

Q99YZ2

O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Song X.T., Feng Z.Q., Guan X.H.;

*Amplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody Schistosoma japonicum.*;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF282622; AAG01452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora;
Trematoda; Digenea; Strigeidida; Schistosomatoidea;
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                                                                                                                  ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
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                                                                                                    IleAsnProSerArgGlyTyrThrAsnTyrAsnGlnLysPheLysAspAr
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Gaps: 1
Percent Identity: 67.213
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Schistosomatidae;
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seq_documentation_block:
ID 09UL70;
AC 09UL70;
PRELIMINARY;
AC 09UL70;
AC 09UL70;
PT 01-MAY-2000 (TrEMBLrel. 13, DT 01-MAY-2000 (TrEMBLrel. 13, DT 01-MAR-2001 (TrEMBUNGIOSE SEQUENCE FROM N.A.

RESEQUENCE FROM N.A.
RESEQUENCE FROM N.A.
RESEQUENCE FROM N.A.
RESEQUENCE FROM N.A.
REDLINE-98277139; PubMed-99 RA Wu X., Liu B., Van der Merra Young D.C.;
RT "Myosin-reactive autoantibust fetus.",
RT "Myosin-reactive autoantibust fetus.",
RT "Myosin-reactive autoantibust fetus.",
RT "Myosin-reactive autoantibust fetus.",
RT "MOSIN-REACTIVE TO IMMUNOG CC -1- SIMILARITY: TO IMMUNOG CC DOMAIN.
DR EMBL; AF035044; AAD56280.1
DR EMBL; AF035044; AAD56280.1
DR HSSP; P01607; 1REI.
DR SMART; SM00406; IGV: 1.
DR SMART; SM00406; IGV: 1.
FT NON_TER 108 AA; 11633
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Quality:
Ratio:
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US-08-487-283A-8 x
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                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin. Immunol. Immunopathol. 87:18-i- SIMILARITY: TO IMMUNOGLOBULIN
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                                        207
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  67
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                                        CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG
                                                                                 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspValA
                                                                                                                         GCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTC
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4.381
89.815
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Gaps: 0
Percent Identity: 77.778
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-08-487-283A-8 x Q9Z1C4
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SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Z1C4
Q9Z1C4;
Q9Z1C4;
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
                                                                      579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 CAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAGCCAGGGGCCTC
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SMART; SM00406; IGv; 1.
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endothelial cells.";
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Mueller J.P., Giannoni M.A., Hartman
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Bohlen H., Diehl V., Wolf J.;
"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated with sommatic mutations within the untranslated regions of rearranged and class switch recombinated Ig genes.";
submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                      GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCGCGAGGTCAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laThrTyrTyrCysGlnGlnSerTyrSerAla...LeuThrPheGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAlaGluAspPheA
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157 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 10, Last sequence update) (TrEMBLrel. 16, Last annotation updat
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letazoa; Chordata; Craniata; Vertebrata; E
letazoa; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                              416.50
4.083
80.952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                                                                                                       Length: 126
Gaps: 1
Percent Identity: 68.254
                                                                                                                                                                                                                                                                                           107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86986EDDA84D88B5 CRC64;
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С
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                                   566
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alignment_block:
US-08-487-283A-8 x
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Quality:
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ID Q9UL79 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                       Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSUL79;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003596; -. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 GlyArgGlyGlyArgTrpArgSerGlyAsn...TyrAsnGlyHisTrpGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   567
            107 ACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF035035; AAD56271.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young D.C.;
                                                                           57 TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGA 106
                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           etus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Myosin-reactive autoantibodies in
                                                                                                   laTrpTyrGlnGlnLysProGlyLysAlaProGluLeuLeuIleTyrAla
                                                 yGlnGlyThrProValThrValSerSer 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAGGAACCCTGGTCACTGTCTCGAGC 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN.
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108 ‡
                                                                                                                                                                                                                                                                                                   AA;
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4.330
87.037
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                                                                                                                                                                                                                                                                                                   11787
                                                                                                                                                       from:
                                                                                                                                                                                                                                                                                                   WW;
                                                                                                                                                                                                                       Length: 108
Gaps: 0
Percent Identity: 75.000
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                                                                                                                                                                                                                                                                                                   DB5845F19724FB4E CRC64;
                                                                                                                                                       to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalis N.N., Berney S.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carditis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
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alignment_block:
US-08-487-283A-8 x Q9QYF0
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                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9QYFO; PRELIMINARY;
Q9QYFO; Q1-mAY-2000 (TrEMBLrel. 1.
01-mAY-2000 (TrEMBLrel. 1.
01-mAR-2001 (TrEMBLrel. 1.
CN 8 SCFV.
CN 8.
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    Q9QYF0 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                          104
                                                                                                              188
                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
SEQUENCE 298 AA; 31867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB036341; BAA88633.1; HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shinohara N., Demura T., Fukuda H.; "Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003006; -.
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                                                                                                                                                                                                                                                                         4
| TGAACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTAC
|| |||||||:::||| ||||||:::|||:::|||||:::|||
| euAlaTrpTyrGlnGlnLysGlnGlyLysSerProGlnLeuLeuValTyr
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                                                                                                                                                                                                                    CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG
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                                                                                                           yGluThrValThrIleThrCysArgAlaSerGlyAsnIleHisAsnTyrL
                                                                                                                                       CGATAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laThrTyrTyrCysGlnGlnTyrTyrSerPheProProThrPheGlyGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:Q9QYF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                             to: Q9QYF0
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4.010
89.381
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16,
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Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Identity:
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                                                                                                                                                                                                                          188
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                                                          153
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SOLUCION SE CONTRA LA CONT
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US-08-487-283A-8 x Q9Y298
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SIGNAL
NON_TER
SEQUENCE
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Q9Y298;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98322155; PubMed=9657749; Jacquemin M.G., Vander Elst L.P.L.; Jacquemin M.G., Vander Elst L.P.L.; "Mechanism and kinetics of factor VIII inactivation: study with ar independent of the partie of the partie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254
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SMART; SM00406; IGv; 1.
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                367 GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAA 416
49
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alignment_scores:
    Quality:
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US-08-487-283A-8 x Q9QXF0
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SEQUENCE
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01-MAY-2000 (TYEMBLIEL 13, Last sequence update)
01-MAR-2001 (TYEMBLIEL 16, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                   529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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SMART; SM00406; IGv; 1.
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                                                               34 etLysTrpValLysGlnSerHisGlyLysSerLeuGluTrpIleGlyAsp
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                              ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                    AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGA 478
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IleAsnProAsnAsnGlyGlyThrSerTyrAsnGlnLysPheLysGlyLy
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117 AA;
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Gaps:
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seq_documentation_block:
ID O9R1A5;
AC O9R1A5;
AC O9R1A5;
AC O9R1A5,
DT O1-MAY-2000 (TrEMBLrel. 13
DT O1-MAY-2000 (TrEMBLrel. 13
DT O1-MAY-2000 (TrEMBLrel. 13
DT O1-MAY-2000 (TrEMBLrel. 16
DE KAPPA LIGHT CHAIN OF MAB7
OS Mus musculus (Mouse).
CC Enkaryota; Metazoa; Chorda
OC Mammalia; Butheria; Rodent
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramod
RT "Cloning of cDNAs encoding
RT antibody (Mab 7, its light
RF Single chain antibody (scr
RL Single chain antibody (scr
RL Submitted (MAY-1999) to th
DR EMBL; AF152371; AAD40242.1
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS00290; IG_MHC;
DR SNART; SM00410; IG_NHC;
DR NOW_TER 214
SQ SEQUENCE 214 AA; 23922
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                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF15.371; AA040242.1;
HSSP; P01789; IMCP.
                                                                                                  107
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InterPro; IPR003600; -.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 rLeuThrValSerSer 117
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                    157
                                                       34 erTrpPheGlnGlnLysProGlyLysSerProLysThrLeuIleTyrArg
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                                                                                                                                     17 uArgValThrIleThrCysLysAlaSerGlnAspIleAsnSerTyrLeuS
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                                                                                                                                                          TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCCTGA
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                                                                                                                                                                                                                   GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGA
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Gaps: 5
Percent Identity: 41.629
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307	CGG	356
101	GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThr 1	114
357		406
115	.ValSerIlePheProProSerSerGluGlnLeuThrSerGlyGlyAla. 1	13(
107	TCCTGTAAAGCTAGCGGC	456
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157	TATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCA	506
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                                  Humanised CDR-grafted 5G1.1 scFv CB (AAR77607) is the product of a DNA construct (AAT08479) derived from DNA of hybridoma ATCC HB 11625, the producer of anti-C5 monoclonal antibody (MAD) 5G1.1. Recombinant scFv CB is obtd. by expression of this DNA in Escherichia coli using vector pET Trc SO5/NI. The light and/or heavy chain CDRs of scFv CB can be combined with CDRs from other 5G1.1-derived antibodies, Fds and light chains (AAR77606-16) in the prodn. of recombinant, including humanised, antibodies that retain the ability of MAD 5G1.1 to block human complement C5a generation and thus to reduce glomerular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                        Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
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Rother RP, Springhorn
Wang Y, Wilkins JA;
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                          inflammation
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antibody; complementarity determining
                                                                                                                                                               Page 110-113; 181pp;
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                        and kidney dysfunction associated with glomerulonephritis
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ibody; antiinflammatory; antibody engine
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Squinto S
                                                                                                                                                               English.
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Thomas TC;
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region; CDR;
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Sequence

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alignment_block:
US-08-487-283A-8 x AAR77607
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 seq_name:
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                        234 yrPheAspValTrpGlyGlnGlyThrLeuValThrValSerSer 248
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                                                                                                                     TGGCGGTGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCG
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                                                                       rAlaValTyrTyrCysAlaArgTyrPhePheGlySerSerProAsnTrpT
                                                                                                                                                                       hr {\tt GluTyrThrGluAsnPheLysAspArgValThrMetThrArgAspThr}
                                                                                                                                                                                                                                                                                                                                                                        yGlyGlyGlySerGlyGlyGlySerGlnValGlnLeuValGlnSerG
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/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR77616
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seq_documentation_block:
ID AAR77616 standard; Protein; 24
XX
AC AAR77616;
XX
DT 15-MAR-1996 (first entry)
XX
DT 15-MAR-1996 (first entry)
XX
Complement C5; haemolysis; kid
KW Complement C5; haemolysis; kid
KW monoclonal antibody; complement
KW single chain antibody; scfv.
XX
Synthetic.
XX
FH Key
FT Region
Jlabel- CDR-L1
FT Region
Jlabel- CDR-L1
FT Region
Jlabel- CDR-L1
 EFFX
                      A humanised CDR-grafted scFv, designated 5G1.1 scFv DO12 (AAR77616), includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The scFv can be expressed in Escherichia coli MEI cells by subcloning of encoding DNA (AAR708488) into vector pET Trc SO5/N1. This humanised, recombinant antibody retained the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
Sequence
                                                                                                                                                                                                               WPI; 1995-392923/50.
N-PSDB; AAT08488.
                                                                                                                                                                                                                                                      Rother RP, Springhorn Wang Y, Wilkins JA;
                                                                                                                                             Example 11; Page 138-140; 181pp; English.
                                                                                                                                                                        component
                                                                                                                                                                                      Treating
                                                                                                                                                                                                                                                                                 Evans MJ,
                                                                                                                                                                                                                                                                                                                                     02-MAY-1994;
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humanised antibody; complementarity determining region; CDR;
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 248
AA;
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225..237
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91..99
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nto SP,
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alignment\_block: US-08-487-283A-8 x

AAR77616

Percent Similarity:

Quality: 1279.00 Ratio: 5.178 milarity: 99.597

Gaps: Percent Identity:

Length:

248 0 97.177

Align seg 1/1

to: AAR77616

from:

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to:

248

alignment\_scores:

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seq_name:
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Complement C5; haemolysis; kidney; glomerulonephritis;
                     Murine 5G1.1M1
                                                                                AAR77606
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                                                                                                          /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR77606
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                                        (first entry)
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EXX DXX XX DXX XX DXX XX DXX

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alignment_block:
US-08-487-283A-8
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                                                                                 Align seg 1/1
                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                Murine scFv 5G1.IM1 (AAR77606) is the product of a DNA construct (AAT08479) obtd. from DNA of hybridoma ATCC HB 11625, which produces anti-C5 monoclonal antibody (MAD) 5G1.1. Recombinant scFv 5G1.IM1 is obtd. by expression of this DNA in Escherichia coli using vector pET Trc SO5/NI. The light and/or heavy chain CDRs of scFv 5G1.IM1 can be combined with CDRs from other 5G1.1-derived antibodies, Fds and light chains (AAR77607-16) in the prodn. of recombinant, including humanised, antibodies that retain the ability of MAD 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                          glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                    Example 11;
                                                                                                                                                                                                                                                                                                                                                                                                           Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALEX-) ALEXION PHARM INC.
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GGGCGATAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCG
                                             ATGGCCGATATCCAGATGACCCAGTCCCCGTCCCTGTCCGCCTCTGT
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                                   MetAlaAspIleGlnMetThrGlnSerProAlaSerLeuSerAlaSerVa
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Ratio: 4.815
milarity: 93.952
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                                                                                  to: AAR77606
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                                                                                                                                                                                                                    248 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Page 107-110; 181pp; English
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seq_name: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:AAW26651
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phagocytosis; tumour infiltration; adhesion; infection; cancer; allergy; rheumatold arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes; graft versus host disease; human; therapy.
                                                                                                                  Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv;
                                                                                                                                                    Chimeric receptor hCTMO1/h/zeta
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                                                                            IgG1: T cell receptor zeta chain; cell proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion;
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alignment_scores:
Quality:
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US-08-487-283A-8 x AAW26651
                                                                                                                                                                             Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                           cytoplasmic signalling components. Also claimed is use of DNA cencoding a recombinant chimeric receptor in a DNA delivery system. The DNA delivery system can be used for the activation of cells to provide e.g. an increase in cell proliferation, expression of cytokines with e.g. pro- or anti-inflammatory responses, stimulation of cytolytic activity, differentiation or other effector functions, antibody secretion, phagocytosis, tumour infiltration and/or infectious disease, inflammatory disease, cancer, allergic/atopic disease, congenital disease, dermatologic disease, transplants and metabolic/idiopathic disease (claimed). In particular, they can be used in the treatment of e.g. cisease, transplants and metabolic/idiopathic disease (claimed). In particular, they can be used in the treatment of rheumatoid arthritis, osteoarthritis, sickle cell anaemia, psoriasis, multiple sclerosis, organ or tissue transplant rejection, graft-versus-host
                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This protein comprises a chimeric receptor consisting of an scFv engineered from anti-CD3 human antibody CTMO1 linked to an extracellular spacer comprising the human IgG1 hinge, part of the extracellular region of human CD28 and 4 amino acid residues, linked to the transmembrane and intracellular regions of the human T cell receptor zeta chain. It can be expressed in host (e.g. Jurkat) cells using a chimeric receptor gene (see AAT90514) constructed from DNA cassettes encoding each component of the receptor. In a claimed cell activation process an effector cell is transformed with DNA encoding a chimeric receptor containing 2 or more different cytolasmic signalling components.
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KW tumour infiltration;
KW rheumatoid arthritis;
KW inflammatory bowel dd
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Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; CD CD26; cell proliferation; cycokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion; infection; cancer; allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes;
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                                                                                                           CD8;
                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC AAT90511) constructed from DNA cassettes of each component. In a CC claimed cell activation process an effector cell is transformed with CC DNA encoding a chimeric receptor containing 2 or more different CC cytoplasmic signalling components. Also claimed is use of DNA CC encoding a recombinant chimeric receptor in a DNA delivery system. CC The DNA delivery systems can be used for the activation of cells to provide e.g. an increase in cell proliferation, expression of cytokines with e.g. pro- or anti-inflammatory responses, stimulation of cytolytic activity, differentiation or other effector functions, antibody secretion, phagocytosis, tumour infiltration and/or increased adhesion. They can be used in the treatment of e.g. C disease, congenital disease, dermatologic disease, congenital disease, dermatologic disease, ransplants and metabolic/diopathic disease, asthma. C eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple c sclerosis, organ or tissue transplant rejection.
                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                 US-08-487-283A-8 x AAW26648
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              sclerosis, organ or tissue transplant rejection, graft-versus-host disease or diabetes (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be expressed in host cells using a chimeric receptor gene (see AAT90511) constructed from DNA cassettes of each component. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein comprises a chimeric receptor consisting of a engineered from anti-CD3 human antibody CTMO1 linked to an extracellular spacer from part of human CD8 hinge, linked extracellular and intracellular components of human CD28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA systems for activating cells - comprising DNA coding chimeric receptor comprising 2 or more different cytoplasmic
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                     103
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                                                                                                                        Similarity:
                                                    pArgValThrIleThrCysArgSerSerLysSerLeuLeuHisSerAsnG
                                                                                       TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCG....
                                                                                                                                                                                                                                                                                                                       Quality:
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seq_name: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:AAW26646
                                                                                                                                                                                                                                                                       .documentation_block:
          Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; CD8; T cell receptor zeta chain; cell proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion; infection; cancer; allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes;
                                                                                                                                                 Chimeric receptor hCTMO1/CD8/zeta
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                                                                                                                                                                                                                                                      AAW26646 standard; Protein; 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluLysPheLysGlyArgAlaThrLeuThrValAspThrSerThrAsnTh
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                                                                                                                                                                                                                                                                                                                                                                                                      heCysAlaArgGluLysThrThrTyrTyrTyrAla...
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human;
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alignment_block:
US-08-487-283A-8 x AAW26646
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                                                                                                                                                                                              Align seg 1/1 to: AAW26646
                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell activation process an effector cell is transformed with DNA encoding a chimeric receptor containing 2 or more different cytoplasmic signalling components. Also claimed is use of DNA encoding a recombinant chimeric receptor in a DNA delivery system. The DNA delivery systems can be used for the activation of cells to provide e.g. an increase in cell proliferation, expression of cytokines with e.g. pro- or anti-inflammatory responses, stimulation of cytolytic activity, differentiation or other effector functions, antibody secretion, phagocytosis, tumour infiltration and/or increased adhesion. They can be used in the treatment of e.g. infectious disease, inflammatory disease, cancer, allergic/atopic disease, transplants and metabolic/idiopathic disease (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This protein comprises a chimeric receptor consisting of an scFv engineered from anti-CD3 human antibody CTMO1 linked to an extracellular spacer in the form of part of human CD8 hinge, linked to the extracellular, transmembrane and intracellular components of the human T cell receptor zeta chain. It can be expressed in host cells (e.g. Jurkat) using a chimeric receptor gene (see AAT90509) constructed from DNA cassettes of each component. In a claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis, osteoarthritis, inflammatory bowel disease, asthma, eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA systems for activating chimeric receptor comprising 2
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 90pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               In particular, they can be used in the treatment of rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-351052/32
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                                                                                                                        21 AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAs
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                                                                                                                                           GATATCCAGATGACCCAGTCCCCGTCCCCTGTCCGCCTCTGTGGGCGA
                                                     pArgValThrIleThrCysArgSerSerLysSerLeuLeuHisSerAsnG
                                                                                      TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCG....
                                                                                                                                                                                                                                                                                                                       Quality:
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seq_documentation_block:
ID AAW26647 standard;
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CD28; T cell receptor zeta chain; cell proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion; infection; cancer; allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes; graft versus host disease; human; therapy.
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                                                                                                                                                     Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; CD8;
                                                                                                                                                                                                  Chimeric receptor hCTMO1/CD8/zeta-CD28
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| LeuLeuMetTyrArgMetSerAsnLeuAlaSerGlyValProSerArgPh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGCGCGCGT.....TATTTTTTGGTTCTAGCCCGAATTGG 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rPheThrAspTyrTyrIleAsnTrpMetArgGlnAlaProGlyGlnGlyL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTTTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC 744
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                                                                                                                                                                                                                                                                                                                                   Protein;
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alignment_block:
US-08-487-283A-8 x AAW26647
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                                                                                                                                                                                                                                                                                                                                                                                                                       cell activation process an effector cell is transformed with DNA
cell encoding a chimeric receptor containing 2 or more different
cytoplasmic signalling components. Also claimed is use of DNA
ce encoding a recombinant chimeric receptor in a DNA delivery system.
ce needing a recombinant chimeric receptor in a DNA delivery system.
ce provide e.g. an increase in cell proliferation, expression of
cytokines with e.g. pro- or anti-inflammatory responses, stimulation
ce of cytolytic activity, differentiation or other effector functions,
ce antibody secretion, phagocytosis, tumour infiltration and/or
increased adhesion. They can be used in the treatment of e.g.
ce increased adhesion. They can be used in the treatment of e.g.
ce disease, congenital disease, dermatologic disease, neurologic
disease, transplants and metabolic/idiopathic disease (claimed).
ce arthritis, osteoarthritis, inflammatory bowel disease, asthma,
ce czema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple.
ce sclerosis, organ or tissue transplant rejection, graft-versus-host
                                                                                                                                                                            Align seg 1/1 to: AAW26647
                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein comprises a chimeric receptor consisting of an scfv engineered from anti-CD3 human antibody CTMO1 linked to an extracellular spacer in the form of part of human CD8 hinge, linked to the extracellular, transmembrane and intracellular components of the human T cell receptor zeta chain, fused to the intracellular component of human CD28. It can be expressed in host cells (e.g. Jurkat) using a chimeric receptor gene (see AAT90510) constructed from DNA cassettes of each component of the receptor. In a claimed cell activation manages an effector cell is transformed with num
                                                                                                                                                                                                                                                                                                                                                                                                          scierosis, organ or
disease or diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-351052/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signalling components.
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                                                                                                    37
                                                                   57
                                                                   TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCG.... 102
                               .....CTGAACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAG
                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                      Ratio:
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4.220
84.906
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Percent Identity:
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seg_name:
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Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; IgG1; T cell receptor zeta chain; cell proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion; infection; cancer; allergy; rheumatcid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psorfasis; multiple sclerosis; transplant rejection; diabetes;
                                                                                                                                              Chimeric receptor hCTMO1/G1/zeta.
                                                                                                                                                                                                                                                       AAW26649 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
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CC cell receptor zeta chain. It can be expressed in host cells (e.g. Jurkat) using a chimeric receptor gene (see AAT90512) constructed CC from DNA cassettes encoding each receptor component. In a claimed CC cell activation process an effector cell is transformed with DNA CC encoding a chimeric receptor containing 2 or more different CC cytoplasmic signalling components. Also claimed is use of DNA CC encoding a recombinant chimeric receptor in a DNA delivery system. CC The DNA delivery systems can be used for the activation of cells to CC provide e.g. an increase in cell proliferation, expression of CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation CC of cytolytic activity, differentiation or other effector functions, CC antibody secretion, phagocytosis, tumour infiltration and/or CC infectious disease, inflammatory disease, cancer, allergic/atopic CC disease, congenital disease, dermatologic disease, neurologic CC disease, transplants and metabolic/idiopathic disease (claimed). CC In particular, they can be used in the treatment of rheumatoid CC arthritis, osteoarthritis, inflammatory bowel disease, asthma, cezema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple CC disease or disheres (claimed). Claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein comprises a chimeric receptor consisting of an scientification anti-CD3 human antibody CTMOI linked to an extracellular spacer comprising the human IgG1 hinge, CH2 and cextracellular spacer comprising the human intracellular regions of the human linked to transmembrane and intracellular regions of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 7; 90pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Homo
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Sequence
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                                     organ or diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        components.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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alignment_block:
US-08-487-283A-8 x
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Quality:
                                                                                                                     Align seg 1/1 to: AAW26649
                                                                                                                                                                                 Percent Similarity:
                      37
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                                                                    TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCG....
                     pArgValThrIleThrCysArgSerSerLysSerLeuLeuHisSerAsnG
                                                                                                                                                                                              Ratio:
.CTGAACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAG 141
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84.906
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seq_name:
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AAW26650 standard;
                         Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; 19G1; CD28; T cell receptor zeta chain; proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion; infection; cancer; allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
psoriasis; multiple sclerosis; transplant rejection; diabetes
                                                                                                                                                                                                                                                                                                                                   Chimeric receptor hCTMO1/G1/zeta-CD28.
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alignment\_block: US-08-487-283A-8 x

Percent Similarity:

Align seg 1/1

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AAW26650 AAW26650

from:

to: 692

GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGA

37

37 57 21

pArgValThrIleThrCysArgSerSerLysSerLeuLeuHisSerAsnG TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCG....  alignment\_scores

Quality: Ratio:

949.50 4.220 84.906

Length: Gaps: Percent Identity:

265 4 70.189

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cassettes encoding each component of the receptor. In a claimed cell activation process an effector cell is transformed with DNA encoding a chimeric receptor containing 2 or more different cytoplasmic signalling components. Also claimed is use of DNA encoding a recombinant chimeric receptor in a DNA delivery system. The DNA delivery systems can be used for the activation of cells to provide e.g. an increase in cell proliferation, expression of cytokines with e.g. pro- or anti-inflammatory responses, stimulation of cytolytic activity, differentiation or other effector functions, antibody secretion, phagocytosis, tumour infiltration and/or infectious disease, inflammatory disease, cancer, allergic/atopic disease, congenital disease, dermatologic disease, neurologic disease, transplants and metabolic/idiopathic disease (claimed). In particular, they can be used in the treatment of rheumatoid artherity forces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein comprises a chimeric receptor consisting of an scFv engineered from anti-CD3 human antibody CTMO1 linked to an extracellular spacer comprising the Human IgG1 hinge, CH2 and CH3, linked to the transmembrane and intracellular components of the human T cell receptor zeta chain, fused to the intracellular region of human CD28. It can be expressed in host cells (e.g. Jurkat) using a chimeric receptor gene (see AAT9033) constructed from DNA constructed from DN
                                                               sclerosis, organ or tissue transplant rejection, disease or diabetes (claimed).
                                                                                                                                  arthritis, osteoarthritis, inflammatory bowel disease, asthma, eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
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chimeric receptor comprising 2 or more
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                                                                                                              A fusion of
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Homo sapiens
             Streptomyces avidinii
                                                           Streptavidin; tumour cell; cancer; adenocarcinoma; hematological malignancy; huNR-LU-10; EGP40; EPCAN
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                                                                                                            single chain antibody/streptavidin.
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                                                                EGP40; EPCAM
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The present sequence encodes a fusion of the single chain antibody thunk-IJ-10 and streptavidin. The antibody binds the antigen EGP40 or EPCAM. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a first nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid, operatively linked to a promoter construct comprises a first nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of or treating. A target site within a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1999;
03-DEC-1999;
Sequence
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431
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alignment_scores:
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                                     151 TACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATC
                                                                                                                101 CGCTGAACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATT
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snLeuAspTrpTyrGlnGlnLysProGlyLysGlyProLysLeuLeuIle
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seq_documentation_block:
ID AAW94269 standard; px
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AC AAW94269;
XX
DT 26-APR-1999 (first e
XX
Trimeric polypeptide;
KW Trimeric polypeptide;
KW fusion protein; ligar
KW artificial antibody;
KW transfection; imagin;
XX
Synthetic.
OS Synthetic.
OS Homo sapiens.
XX
PN W09856906-A1.
XX
PN W09856906-A1.
XX
PD 17-DEC-1998.
XX
PF 11-JUN-1998; 98W0-1
XX
PR 11-JUN-1997; 97DK-0
XX
PA (ETZE/) ETZERODT M.
PA (ETZE/) ETZERODT M.
                                                                                                                                                                                                                                                                 fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CEA6.
                                                                                                                                                                                                                                                                                                                                                             H6FXscFv(CEA6)tripBscFV(CEA6) fusion protein sequence
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   (GRAV/) GRAVERSEN N J H.
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snThrLysSerAspLeuSerPheGlnGlyArgValThrIleThrAlaAsp
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|TGlySerGlySerAspTyrThrLeuThrIleSerSerLeuGlnProGluA
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Sequence

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molety, the TYSE being capable of forming a stable complex with 2 other TYSEs, with the proviso that the heterologous molety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN123 (AAW94261 to AAW94264). The TYSE can be used for the construction of conjugates with heterologous moleties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive molety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent entities for generating chimeric artificial antibodies having preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous
                                  population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXscFv(CEA6)tripBscFv(CEA6) fusion protein sequence encoded by the plasmid pH6FXscFv(CEA6)tripBscFV(CEA6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOLT/)
(KAST/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprise a tetranectin trimerising structur linked to at least one heterologous moiety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monomer polypeptide constructs comprise a tetranectin trimerising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larsen IK, Nielsen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Etzerodt M,
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KASTRUP J S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graversen
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R. Thogersen !
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ogersen HC;
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alignment_block:
US-08-487-283A-8
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                                                  204
                                                                                 154
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                                                                                                                                  104 TGAACTGGTATCAACGTAAACCTGGGGAAAGCTCCGAAGCTTCTGATTTAC
                                                                                                                                                                                                                                                 {\tt 170.yAspArgValThrIleThrCysArgAlaSerGluGlyIleTyrHisTrpL}
                                                                                                                                                                                                  54 CGATAGGGTCACCATCACCTGCGGCGCCAGCAAAACATCTATGGCGCGC 103
                                                                                                                                                                                                                                                                                   4 GCCGATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGG
CTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACT
                                                                   GGTGCGACGAACCTGGCAGATGGAGTCCCTTCTCGCCTTCTCTCTGGATCCGG
                                                 LysAlaSerSerLeuAlaSerGlyAlaProSerArgPheSerGlySerGl
                                                                                                                 euAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyr
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documentation_block:
AAR20185 standard; peptide;
                                                 Sequence of the shortened hinge version chain Fv hinge.
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Home.
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                         Fv fragment;
                                                                                         15-APR-1992
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                                                                                                                                                                                                                                                        yrGluLeuTyrTyrTyrMetAspValTrpGlyGlnGlyThrMetVal
                                                                                                                                                                                                                                                                                                                                                                                                                            GCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt GlyGlyThrLysLeuGluIleLysArgAlaAlaAlaGluGlnLysLeuIl}
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                                                                                                                                                                                                         ThrValSerSer 453
                                                                                                                                                                                                                                 ACTGTCTCGAGC 744
                                                                                                                                                                                                                                                                                                        CACGGCCGTCTATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCCGAAT. 696
                                                                                                                                                                                                                                                                                                                                                            {\tt GluSerThrSerThrAlaTyrMetGluLeuSerSerLeuArgSerGluAs}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                             hr \verb|AlaAsnTyrAlaGlnLysPheGlnGlyArgLeuThrIleThrAlaAsp|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaSerGlyGlyThrPheSerAsnSerProIleAsnTrpLeuArgGlnAl
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sapiens
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                          'n
                                                                                        (first entry)
                         Vivo
                        diagnosis;
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                         therapy; antibody
                                                              of
                                                                the B72.3
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alignment_block:
US-08-487-283A-8 x AAR20185
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                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAR20185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The bivalent antigen-binding protein B72.3 FV (AAR20184) is an example of the antigen-binding proteins of the invention. They comprise a first FV fragment bound to at least one other FV fragment by a linker which keeps the FV fragment apart. The connecting structure of AAR20184 comprises a joining sequence derived from a human IgG1 domain linked to a complete human IgG4 hinge region. AAR20185 is the sequence of the shortened hinge version of the B72.3 single chain FV
                        105
                                                                                                                                                  204 CTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACT
                                                                                                                                                                                          New multivalent antigen-binding proteins - comprise Fv fragment linked to at least 1 other Fv fragment spacer and useful for in-vivo diagnosis or therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1990;
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                                                     304 CAGGGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGG
                                                                                                           254 TCGCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGA
                                                                                                                                                                                                                                                                            104 TGAACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTAC
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                                                                                                                                                                                                                                                                                                                    54 CGATAGGGTCACCATCACCTGCGGCGCCAGAAAACATCTATGGCGCGC
                                                                                                                                                                                                                                                                                                                                                          CGGTGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCG
                                                                               y \verb|GluThrValThrIleThrCysArgAlaSerGluAsnIleTyrSerAsnL|
                                                                                                                                                                                                                                                 euAlaTrpTyrGlnGlnLysGlnGlyLysSerProGlnLeuLeuValTyr
                                                                                                                                     ySerGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnSerGluAspP
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4.123
84.211
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Gaps: 2
Percent Identity: 66.397
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present sequence represents a fusion which is used in the exemplification

protein designated apoptobody3sc, of the present invention.

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seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
The present invention describes a method for causing apoptosis in whi a fused gene consisting of a gene participating to apoptosis and a genecoding at least the variable region of anti-idiotype antibody is transfected to a cell to express the fused gene and then an idiotype antibody is reacted with the expressed cell. The method is useful in medical, pharmaceutical, pharmacological and biochemical fields. The
                                                                                                                                                                                                                                                                               (HAGI/)
                                                                                                                            Disclosure; Page 8-9; 10pp; Japanese.
                                                                                                                                                                                      Causing
                                                                                                                                                                                                                                                                                                                                      29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion
medical; pharmaceutical; pharmacological; biochemical.
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                                                                                                                                                                                                                                         2000-332086/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:AAY91026
                                                                                                                                                                apoptosis comprises transfecting cell with idiotypic antibody -
                                                                                                                                                                                                                                                                             HAGIWARA Y.
HAGIWARA H.
                                                                                                                                                                                                                          AAA39167
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| GlyThrLySLeuGluIleLySArgAlaAspAlaAlaProThrValSerLe
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ATTTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGA 723
                    {\tt gSerLeuThrAsnGluAspSerAlaValTyrPheCysThrLysGluGluT}
                                          CAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCGCGT.....T
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seq_name: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:AAY43749
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The present sequence represents a bscCD19xCD3 antibody. This antibody is a bispecific single-chain polypeptide comprising domains providing binding-site of immunoglobulin chains or antibodies specifically recognizing CD19 and CD3 antigen. The polypeptide destroys CD19-positive target cells without any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic T-lymphocytes and so specific lysis by T-cells rather than a direct effect by an antibody is achieved. The bispecific single-chain polypeptides, or nucleotides encoding them, are used for the treatment of B-cell malignancies, B-cell mediated autoimmune diseases like myasthenia gravis, Morbus Basedow, Hashimoto thyroiditis or Goodpasture syndrome or for the depletion of B- cells and more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bscCD19xCD3
CD3 antiqen:
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                                                                                                                                                                                    especially non-Hodgkin lymphoma
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283..401
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526..53
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28..138
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                   595 GACACTTCGACTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGA
                                                                                                                                                                                                                                                                           445 AAAGCTAGCGGCTATATTTTTTCTAATTATTGGATTCAATGGGTGCGTCA
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seq_documentation_block:
ID AAY59264 standard; pp
AC AAY59264;
XX AAY59264;
XX 17-APR-2000 (first 6
XX Antibody 4H5 H chain
XX CD4 antigen; anti-hun
XX CD4 antigen; anti-hun
XX JP11332563-A.
XX JP11332563-A.
XX JP11332563-A.
XX 26-MAY-1998; 98JP-(
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"Isolation of the major outer-membrane protein of Actinobacillus pleuropneumoniae and Haemophilus parasuis.";

J. Vet. Med. B 42:59-63(1995).

-i- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.

-i- SUBUNIT: DISULFIDE BONDS INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS

-i- SUBCELLULAR TICATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.

OUTER COMPONENTS FORM HIGH MOLECULAR MEMBRANE.

OUTER COMPONENTS FORM HIGH MOLECULAR MEMBRANE.

OUTER MEMBRANE POTIN.

OUTER MEMBRANE POTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94350802; PubMed=8071198;
Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.
"Phylogeny of mycoplasmalike organisms (phytoplasmas): a basis
their classification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002222; ... PROSITE; PS00323; RIBOSOMAL S19; PARTIAL.
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-i- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STR
-i- TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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HGHTKDSK 9
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Pred. No. 7.1e
3; Mismatches
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                                                                                                                                                                                              Score 23; DB 1;
Pred. No. 6.8e+02
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1 01-NOV-1988 (Rel. 09, Created)

I 01-NOV-1988 (Rel. 09, Last sequence updated)

I 01-PEB-1995 (Rel. 31, Last annotation updated)

T 01-FEB-1995 (Rel. 31, Last annotation updated)

TOTTOPPACYCLINE RESISTANCE LEADER PEPTIDE.
                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                 Leader peptide; A SEQUENCE 20 AA;
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PIR;
                                                                                                                                                                                                                                                          EMBL; D00006; BAA00004.1; -. EMBL; M11036; AAA22850.1; -. EMBL; X51366; CAA35750.1; -. EMBL; X60828; CAA43219.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schwarz S., Cardoso M., Wegener H.C.;
"Nucleotide sequence and phylogeny of the tet(L) tetracycline resistance determinant encoded by plasmid pSTE1 from Staphylogens."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
"Nucleotide sequence of the tetracycline resistance gene of p
thermophilic Bacillus plasmid: comparison with staphylococcal
controls.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus hyicus.
Plasmid pTHT15, Plasmid pBC16, and Plasmid Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90221899; PubMed-2109312;
Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;
"Nucleotide sequence of the tetracycline resistance gene of pBC16
from Bacillus cereus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 37:131-138(1985).
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MEDLINE=86031344; PubMed=2996983;
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NCBI_TaxID=1422, 1396, 1284;
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S23742; S23742.
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                                                                                                                       Conservative
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                                                                                                                                                                                                 Antibiotic resistance; Plasmid.
A; 2253 MW; 18D0F4A6CA231CA1 CRC64;
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Pred. No.
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15-DEC-1998 (Rel. 15-DEC-1998 (Rel. 15-DEC-1998 (Rel. 15-DEC-1998 (Rel. EARLY NODULIN 40.
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UNKNOWN PROTEIN CP
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SEQUENCE 17 AA; 20
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                  Nodulation
                                     EMBL; AF013594;
                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                use
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                                                                                                                                                                                                                                                                                                                                                                      Chian R.-J.,
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. GIFU;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=34305;
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MEDLINE=98291870;
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"Isolation and Primary characterization
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                                                                                      s SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as i
ified and this statement is not removed. Us
ities requires a license agreement (See http
                                                                                                                                                                                                                                                        lation and ramme, is japonicus cultivar 'Gifu'."; is japonicus cultivar 'Gifu'."; plant Gene Register PGR97-142.
FUNCTION: MODULATES THE ACTION OF AUXIN, A PORTICATOR THAT ALTERS PHYTOHORMONE
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Query Match Best Local Similarity

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O24369;
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P55959;
01-NOV-1997
                           Eukaryota; Viridiplantae; Embr
Magnoliophyta; eudicotyledons;
Fabales; Fabaceae; Papilionoid
                                                          Pisum sativum (Garden
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SEQUENCE FROM N.A
                 NCBI_TaxID=3888;
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Fabales; Fabaceae; Papilionoideae;
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FUNCTION: MODULATES THE ACTION
GROWTH REGULATOR THAT ALTERS PI
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                                                                                                                                                                                                                                                                                                                                MEDLINE-96011756; PubMed-7548828;
Vijn I., Yang W.-C., Pallisgaard N., Oestergaard Jensen E.,
van Kammen A., Bisseling T.;
"VSENOD5, VSENOD12 and VSENOD40 expression during Rhizobium-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vicia sativa (Spring vetch) (Tare).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed during both early and late stages of nodule development."; plant Mol. Biol. 26:487-493(1994).
-!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
                                                                                                                                                                                                                                                                                               nodule formation on Vicia sativa roots."; Plant Mol. Biol. 28:1111-1119(1995).
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DEVELOPMENTAL STAGE: EXPRESSED DURING RHIZOBIUM-INDUCED NODULE FORMATION. IN 4-DAY OLD NODULES IT IS FOUND IN ALL THE CELLS OF THE CENTRE OF THE NODULE PRIMORDIUM AND ALSO OCCURS IN THE REGION OF THE ROOT PERICYCLE FACING THE NODULE PRIMORDIUM. AT DAY 5. EXPRESSION IS SEEN IN THE COMPLETE CENTRAL TISSUE. AT DAY 20 EXPRESSED IN THE COMPLETE PREFIXATION ZONE II, AND IN THE PROXIMAL PART OF THIS ZONE IT IS FOUND DALY IN THE INFECTED CELLS BUT NOT IN THE UNINFECTED CELLS. AT THE TRANSITION OF PREFIXATION ZONE II INFO INTERZONE II-III EXPRESSION DECREASES IN THE INFECTED CELLS. IN THE PROXIMAL PART OF THIS ZONE IT IS UNIDUCED IN THE UNINFECTED CELLS. AND IN THE PROXIMAL PART OF THIS ZONE IT IS UNDETECTABLE. IN THE PROXIMAL PART OF THIS ZONE IT IS UNDETECTABLE.
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P81358;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
                                                                                                           _CLOPA
Clostridium pasteurianum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
UNKNOWN PROTEIN CP 37 FROM 2D-PAGE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                         binding properties to synaptosomal membrane K+ channels.";
Biochem. Int. 27:953-962(1992).
-i- FUNCTION: BLOCKER OF POTASSIUM CHANNELS.
-i- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM CHANNEL INHIBITORS SUBFAMILY.
Interpro; IPRO01947; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leiurus quinquestriatus quinquestriatus (Egyptian scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Leiurus.
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Valdivia H.H., Martin B.M., Escobar L., Possanı ı
Valdivia H.H., Martin B.M., Escobar L., Possanı ı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Venom;
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NCBI_TaxID=1501;
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Plengsrud R., Skjeldal L.;

"Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5 electrophoresis 19:802-806(1998).

-i- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKY PROTEIN IS: 5.8, ITS MW IS: 44.7 KDA.
MISGURIN.
Misgurnus anguillicaudatus.
Eukaryota; Metazoa; Chordata; Craniata;
Eutaryota; Mecazoa; Chordata; Teleostei;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cobitidae; Misgurnus.
NCBL_TaxID-75329;
[1]
                                                                                                                                                                                                                                                        MISAN
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NON_TER
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asterio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tejera M.L., Villalba M., Rodrig "Isolation and characterization tree pollen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
POLLEN ALLERGEN OLE E 7 (OLE E VII) (FRAGMENT).
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P37723;
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OMP4_PASHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.;
"A novel antimicrobial peptide from the loach, Misgurnus
anguillicaudatus.";
FEBS Lett. 411:173-178(1997).
-i- FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL
GRAM-POSITIVE AND GRAM-NEGARTIVE BACTERIA AND FUNGI.
-i- MASS SPECTROMETRY: MW-2502; METHOD-MALDI.
Antibiotic; Fungicide.
                                                                                                                                    LT 15
SALTY
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01-NOV-1995
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NON_TER 21 21
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MEDLINE=95102227; PubMed=7803929;
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01-NOV-1995
SEQUENCE FROM N.A.
                   NCBI_TaxID=602;
                                         Bacteria; Proteobacteria;
                                                   Salmonella typhimurium
                                                                                                                                                                                                                                                                                                     Int. J. Med. Microbiol. Virol. Parasitol.
-!- SUBUNIT: MONOMER (PROBABLE).
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MEMBRANE PROTEIN P44 (OMP) (FRAGMENT)
haemolytica
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2; Mismatches
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                                          subdivision; Enterobacteriaceae;
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Robison K., Gilbert W., Church G.M.;
"Large scale bacterial gene discovery by similarity search.";
Nat. Genet. 7:205-214(1994).
-i- FUNCTION: PROVIDES RESISTANCE TO OSMOTIC STRESS. MAY BE IMPORTANT
FOR STATIONARY-PHASE SURVIVAL.
-i- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
                                                                                                                                                                                                                                     Membrane; Lipoprotein.
NON_TER 1 1
SEQUENCE 20 AA; 179
                                                                                                                                                                                                                                                                                     EMBL; x05382; -; NOT_ANNOTATED_CDS.
StyGene; SG10272; osmB.
InterPro; IPR000437; -.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87190435; PubMed=2436909;
Theisen M., Kelln R.A., Neuhard J.;
"Cloning and characterization of the pyrF operon of Salmonella typhimurium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANCHOR (PROBABLE).
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein protein search, using sw model

July 19, 2001, 07:46:49; Search time 12.72 Seconds (without alignments) 125.760 Million cell updates/sec

Perfect score: US-08-487-283A-1 107

Sequence:

1 VIDHQGTKSSKCVRQKVEGSS

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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4046

Maximum B B seq length: 0 length: 21

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

28 29	200	24	22 23	21	19 20	18	17	16	15	14	13	12	11	10	9	8	7	σ	ъ	4	ω	2	<u>.</u>	Result
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mitogen regulated pollen allergen Fe	major outer membra annexin VI homolog	fibrinopeptide A - glycine cleavage s	synaptosomal-assoc	hypothetical E2 pr	manganese peroxida T-cell receptor al	beta 3-adrenergic	glutathione dehydr	major outer membra	Ig heavy chain DJ	Ig kappa chain J s

## ALIGNMENTS

RESULT 2
PH.1582
Ig H chain V-D-J region (wild-type clone 5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999
C;Accession: PH1582
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less
A;Reference number: PH1580; MUID:93301809
A;Accession: PH1582 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m A;Reference number: PH1580; MUID:93301609
A;Accession: PH1589 RESULT 1

PH1589

Ig H Chain V-D-J region (wild-type clone 140) - mouse (fragment)

C; Species: Mus musculus (house mouse)
C; Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999
C; Accession: PH1589

R; Levinson, D.A.; Campos-Torres, J.; Leder, P. A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin A; Molecule type: DNA A; Residues: 1-16 <LEV> A; Experimental source: bone marrow C; Keywords: immunoglobulin 밁 δÃ Query Match
Best Local Similarity
Matches 4; Conserv Query Match 28.0 Best Local Similarity 55.6 Matches 5; Conservative 12 CVRQKVEGS 20 12 CVRQKVEGS 20 1 CARQSYDGS 9 Conservative 23.48; 28.0%; Score 25; DB 2; Pred. No. 1.1e+03 2; Mismatches 1; Score 30; DB 2; Pred. No. 1.8e+02; pre-B lymphocyte Mismatches Length 15; Length 16; Indels Indels 0; 0 Gaps Gaps 0 0

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C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C;Accession: $02808
R;Sapp, M.; Richter, A.; Weisshart, K.; Caizergues-Ferrer, M.; Amalric, F.; Wallace, M. Bur. J. Biochem. 179, 541-548, 1989
A;Title: Characterization of a 48-kba nucleic-acid-binding fragment of nucleolin.
A;Reference number: $02808; MUID:89153087
A;Accession: $02808
A;Molecule type: protein
A;Residues: 1-19 <SAP>
                                                                                                                                    R.McHeyrer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V. J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607
A;Accession: PH1675
A;Accession: PH1675
A;Molecule type: mRNA
A;Residues: 1-12 <MCH>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1675
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: $45373
R;Marty, I.; Brugidou, C.; Chartier, Y.; Meyer, Y.
Plant J. 4, 265-278, 1993
A;Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts.
A;Reference number: $45372; MUID:94035181
A;Accession: $45373
A;Status: preliminary
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A;Residues: 1-18 <MAR>
A;Cross-references: EMBL:Z14080; NID:g443955; PIDN:CAA78458.1; PID:g443956
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'Pred. No. 1.9e+03;

3; Mismatches 0;
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                                                                     Eur. J. Immunol. 24, 1657-1664, 1994
A.Title: Entry of B lymphocytes into the persistent cell
A; Reference number: I53392; MUID:94298870
A; Accession: I67525
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C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1676
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                A; Molecule type: mRNA
A; Residues: 1-15 < RES>
                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                           R; Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
                                                                                                                                                                                  C; Accession: I67525
                                                                                                                                                                                            C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998
                                                                                                                                                                                                                                      CD33 antigen homolog - mouse (fragment)
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A; Residues: 1-14 < MCH>
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J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B_cell_differentiation in vivo.
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A; Residues: 1-13 <MCH>
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A;Cross-references: GB:S71349; NID:g550037
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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C. Genomics 13, 999-1007, 1992
A;Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile A;Reference number: A43284; MUID:92372070
A;Accession: D45193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 01-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: D45193
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A; Residues: 1-16 < LIC>
A; Cross-references: GB. M88369; NID: 9340475; PIDN: AAA61327.1; PID: 9340476
A; Note: sequence extracted from NCBI backbone (NCBIN: 111662, NCBIP: 111664)
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A; Gene: Ig VH7183
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A; Residues: 1-17 <STO>
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                                                                                                                                                                                          Gene: F14D16.5
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Best Local
                                                Matches
                                                                                                                                                                    position:
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les 4; Conserv
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4 HQGTKSSKC 12
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                                             Score 23; DB 2; Le
Pred. No. 2.6e+03;
2; Mismatches 3;
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Pred. No. 2.5e+03;
0; Mismatches 5
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Pred. No. 2.3e+03
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C;Species: Legionella pneumophila
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Mar-1996
C;Accession: A44927; B44927
R;Hoffman, P.S.; Seyer, J.H.; Butler, C.A.
J. Bacteriol. 174, 908-913, 1992
A;Title: Molecular characterization of the 28- and 31-kilodalton subunits o A;Reference number: A44927; MUID:92121130
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A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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A;Recession: PH1621
A;Molecule type: DNA
A;Residues: 1-18 <LEV>
A;Residues: 1-18 <LEV
A;Residues:
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c;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_cha
C;Accession: PH1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
A; Gene: SPBC2G2.18;
A; Map position: 2
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A; Residues: 1-19 <LYN>
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C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50329
                                          A; Reference number: A; Accession: A44927
                                                                                                                                                                                                                                                                                                                                                                                                                    major outer membrane protein 28K chain – Legionella pneumophila (fragment) N;Alternate names: major outer membrane protein 31K chain
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A; Status: preliminary
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Matches 5; Conserv
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Pred. No.
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Pred. No. 2.9e+03;
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2.7e+03;
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A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607
A;Accession: PH1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (clone NP-7-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
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A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular cha;Reference number: S19532; MUID:92106333
A;Accession: S19618
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C;Species: Eudistylia vancouveri
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
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A; Residues: 4-17 <HO2>
A; Residues: 1-17 <HO2>
A; Experimental source: SVir Philadelphia 1, serogroup 1
A; Note: sequence extracted from NCBI backbone (NCBIP:77837)
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A; Residues: 1-21 <MCH>
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                            Score 23; DB 2;
Pred. No. 3.2e+03;
3; Mismatches 0
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Pred. No. 3e+03;
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Search completed: July 19, 2001, 07:47:53 Job time:  $64\ \text{sec}$ 

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/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-U8-121-U34C-3U + /22.3U 1346.20 4 6.6-68 244 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-230-843-2 + 777.50 1322.63 12e-66 244 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-636-936-2 + 777.50 1322.63 12e-66 244 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-636-936-2 + 777.50 1322.63 12e-66 244 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-862-124-14 + 771.50 1310.07 - 4.7e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-863-124-14 + 764.00 1299.48 2.3e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-636-936-4 + 764.00 1299.48 2.3e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-636-936-4 + 764.00 1299.48 2.3e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-661-174A-2 + 763.50 1298.79 2.5e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-661-174A-2 + 763.50 1299.48 2.3e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-661-174A-2 + 763.50 1299.48 2.3e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-661-174A-2 + 763.50 1299.48 2.3e-65 243 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-661-174A-2 + 763.50 1299.49 2.5e-65 263 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-297-772A-6 + 751.50 1277.64 3.6e-64 252 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-297-772A-6 + 751.50 1277.64 3.6e-64 252 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-655-906-25 + 726.00 1232.02 1.1e-61 30 /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-392-338A-19 + 692.00 1168.77 2.2e-58 48 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-09-166-093-19 + 692.00 1168.77 2.2e-58 48 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-09-166-093-19 + 692.00 1168.77 2.2e-58 48 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-09-166-094-19 + 692.00 1168.17 4.4e-58 26 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-09-166-094-19 + 692.00 1168.17 4.4e-58 26 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-09-166-094-19 + 692.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database: Issued_Patents_AA:*
Database sequences: 193259
Database length: 20144635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search time (sec): 23.060000
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                                                                                             cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-323-445A-8
cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-515-903A-8
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=tra.rai
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-LOOPEXT=0.000 -QGAPOD=4.500 -QGAPEXT=0.050 -XGAPOD=10.000
-XGAPEXT=0.500 -FGAPOD=6.000 -FGAPEXT=7.000 -YGAPOD=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOD=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOD=0.000
-YGAPOD=0.000 -YGAPOD=0.000 -YGAPOD=0.000
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-OUTEWT-pfs -NORM-ext -MINLEN=0 -MAXLEN=2000000000
-USER-US08487283_@CGN1_1_33 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLP
                                                                                                                                                                                      2_6/ptodata/2/iaa/5A_COMB.pep:US-08-515-903A-4 +
2_6/ptodata/2/iaa/PCTUS_COMB.pep:PCT-US95-12840-4
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                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-487-283A-8 x US-08-488-113B-147
                                                                                                                                                                                                                                                                                   alignment_scores:
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CITY: C
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; MOLECULE TYPE: US-08-488-113B-147
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-765-469-1
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    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07 FILING DATE: 19-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP-DEC-FILING DATE: 09-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/425,336 FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/488,113B FILING DATE: 07-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                Quality:
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                                                                                                                                                                                                                                                                                                                                                         amino acid
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MCNIChOlas, Janet M.
MCNICHOLAS
                                            Ratio:
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                                                                                                                                                                                                                                                                                                                     linear
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O West Madison Street, 34th floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/988,430
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Align seg 1/1

to: US-08-488-113B-147

from: 1

to: 240

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seq_documentation_block:
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                                                                                             Sequence 147, Application US/08477484B Patent No. 5756699
                                                                           GENERAL: INFORMATION:
                       APPLICANT:
APPLICANT:
APPLICANT:
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132 lyLeuValLysProGlyGlySerValArgIleSerCysAlaAlaSerGly 148
       TITLE OF INVENTION:
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                                                                                                                                                                                                ATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGA 106
                                                                                                                                                                                                                                                                                                           CTATTATTGCGCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTATTTTG 706
                                                                                                                                                                                                                                                                                                                                            AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGT 656
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                                                                                                                                                                                                                                                                   lTyrPheCysThrArgArgGlyTyr.....AspTrpTyrPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sGlyLeuGluTrpMetGlyTrpIleAsnThrHisThrGlyGluProThrT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yGlySerGlyGlyGlySerGluIleGlnLeuValGlnSerGlyGlyG 132
                                                                                                                                                                                                                                                                                                                                                                                                                yralaaspSerPheLysGlyargPheThrPheSerLeuaspaspSerLys 198
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Studnika, Gary M.
VENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                        Better, Marc D.
                                                                                                                                                                                                                                                                                                                                            215
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US-08-487-283A-8 x US-08-477-484B-147
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNIcholas, Janet M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 12-MAY-1993

PRIOR APPLICATION UNDER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
                                                        107 ACTGGTATCAACGTAAACCTGGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
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APPLICATION NUMBER: US 08/425,336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 169 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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157 GCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTC 20t
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                                34 erTrpPheGlnGlnLysProGlyLysAlaProLysThrLeuIleTyrArg
                                                                                                                                                 57 TAGGGTCACCATCACCTGCGGCGCCCAGCGAAAACATCTATGGCGCGCTGA 106
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CLASSIFICATION:
                                                                                                                                                                                                     7 GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                    1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/477,484B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 lyLeuValLysProGlyGlySerValArgIleSerCysAlaAlaSerGly 148
                                                                                                                                                                                                                                                       TITLE OF INVENTION: IM
TITLE OF INVENTION: Pr
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 AGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GlyThrLysLeuGluMetLys.....GlyGlyGlyGlySerGlyGlyGl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG
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CITY: Chicago
                                                                                                                                                           COUNTRY:
  APPLICATION NUMBER:
                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCCG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTTGGTGGCGG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrAlaAspSerPheLysGlyArgPheThrPheSerLeuAspAspSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lTyrPheCysThrArgArgGlyTyr.....AspTrpTyrPheA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-646-360-147
                                                                                                                                        60661
                                                                                                                                                                             Illinois
                                                                                                                                                                                                                    E: McAndrews, Held & Malloy, Ltd. 500 West Madison Street, 34th floor
                                                                                                                                                             USA
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173
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  US/08/646,360
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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-646-360-147 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
                                                                           307
                                                                                                                                                                                                                                                                                                                                                                             107 ACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 04-NOV-1991
                                        101
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APPLICATION NUMBER:
  357
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GATATCCAGATGACCCAGTCCCCGTCCCTGTCCGCCTCTGTGGGGGGA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                    CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG
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                                                                                                                                                       CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                    GCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs
TGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCCG
                                      GlyThrLysLeuGluMetLys.....GlyGlyGlyGlySerGlyGlyGl
                                                                                                                  lyIleTyrTyrCysGlnGlnTyrAspGluSerProTrpThrPheGlyGly 100
                                                                                                                                                                                                                                                                                                                                                             erTrpPheGlnGlnLysProGlyLysAlaProLysThrLeuIleTyrArg
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Percent Identity:
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165 507 149 457

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115 357 307

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199
                                                                                                                                         APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                     PRIOR APPLICATION DATA:
                                                                               PRIOR, APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 500 West
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                     APPLICATION NUMBER: US 0: FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
  APPLICATION NUMBER:
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|TyrPheCysThrArgArgGlyTyr......AspTrpTyrPheA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                      US 07/988,430
  US 07/787,567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-839-765-147
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 mnino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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ATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT 606
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312/707-9155
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4.105
84.959
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1991
Percent Identity: 66.667
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US-08-487-283A-8 x US-08-839-765-147

207 CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG rGlyThrAspTyrThrLeuThrIleSerSerLeuGlnTyrGluAspPheG 256 84

67

257 CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 84 lylleTyrTyrCysGinGlnTyrAspGluSerProTrpThrPheGlyGly 100

457 TATATTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCA 506 TyrThrPheThrAsnTyrGlyMetAsnTrpValArgGlnAlaProGlyLy

507 GGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAAT 556 sGlyLeuGluTrpMetGlyTrpIleAsnThrHisThrGlyGluProThrT

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seq_documentation_block:
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                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 147:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Chicago
CITY: Chicago
TITE: Illinois
                                                                                                                                                                         APPLICATION NUMBER: US 07/787,567
FILLING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCMicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/1
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
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ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
              SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/6 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lTyrPheCysThrArgArgGlyTyr.....AspTrpTyrPheA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/US94/05348
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alignment_block:
US-08-487-283A-8 x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-136-389-147 from: 1
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                                                                                                                                                                                                                                                                                                                132 lyLeuValLysProGlyGlySerValArgIleSerCysAlaAlaSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                      407 AGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 erTrpPheGlnGlnLysProGlyLysAlaProLysThrLeuIleTyrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs
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                                                                                                    ATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC 744
                                                                                                                                                                        yrAlaAspSerPheLysGlyArgPheThrPheSerLeuAspAspSerLys 198
                                                                                                                                                                                                                                              sGlyLeuGluTrpMetGlyTrpIleAsnThrHisThrGlyGluProThrT
                                                                                                                                                                                                                                                                                GGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAAT
                                                                                                                                                                                                                                                                                                                                                    TATATTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATCTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lyIleTyrTyrCysGlnGlnTyrAspGluSerProTrpThrPheGlyGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG
                                   lTyrPheCysThrArgArgGlyTyr.....AspTrpTyrPheA
                                                                    CTATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCCGAATTGGTATTTTG
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84.959
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Identity:
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66.667
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spValTrpGlyGlnGlyThrThrValThrValSerSer 240

seq\_name: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:US-08-400-115-4

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alignment_block:
US-08-487-283A-8 x US-08-400-115-4
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                                                                                                                                                       Align seg 1/1 to: US-08-400-115-4 from: 1
                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRILICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,136
FILING DATE: 27-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,193
APPLICATION DATE: 17-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5864019
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 040283/0106 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/GB91/00935
FILING DATE: 11-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9012995.8
FILING DATE: 11-JUN-1990
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OWENS, Raymond John APPLICANT: YARRANTON, Geoffrey Thomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                 54 CGATAGGGTCACCATCACCTGCGGCGCCAGCAAAACATCTATGGCGCGCC 103
                                                                         22 AlaAspIleGlnMetThrGlnSerProAlaSerLeuSerValSerValG1 38
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: ISACSON, John P
REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3000 K Street, N.W., CITY: Washington, D.C.
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yGluThrValThrIleThrCysArgAlaSerGluAsnIleTyrSerAsnL 55
                                                                                                                 GCCGATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              271 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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4.123
84.211
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Percent Identity: 66.397
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seq_documentation_block:
; Sequence 41, Applicati
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                                                                                                                                                                                                                                                                                                          Patent No. 6045793
GENERAL INFORMATION:
                                                                                                                                                                         APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                  APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 .....TrpGlyGlnGlyThrThrLeuThrValSerSer
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                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 TTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC
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                                                                            STREET: Two Embarcac
CITY: San Francisco
                                                                 STATE:
                        ZIP: 94111-3834
                                        COUNTRY:
                                                                                                                              ADDRESSEE:
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                                                                 California
                                                                                                          Two Embarcadero Center, Eighth
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alignment_block:
US-08-487-283A-8 x US-08-875-811-41
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REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amii
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
APPLICATION NUMBER: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fails, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                 101
                                            115
                                                                                                                                                                       307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGG 356
                                                                                                                                                                                                                                                                                                                                                                                                                  157 GCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTC 206
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407 AGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGC
                                                                                                                                                                                                                                                        257 CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                                               207 CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG 256
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TYPE: amino acid.
TYPE: inear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
COMPUTER: II
                                                                                                                             AspIleLysMetThrGlnSerProSerSerMetTyrAlaSerLeuGlyGl
                                        TGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCC 406
                                                                                                                                                                                                                  lyIleTyrTyrCysLeuGlnTyrAspGluPheProTyrThrPheGlyGly 100
                                                                                                                                                                                                                                                                                                                                                                                          AlaAsnArgLeuValAspGlyValProSerArgPheSerGlySerGlySe
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                                                                                                                                                                                                                                                                                                       rGlyGlnAspTyrSerLeuThrIleSerSerLeuGluTyrGluAspMetG
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3.938
82.114
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seq_documentation_block:
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                                                                                                                                                     FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
THE LEBOURE: 41,718, YS-6,0200
                                                                                            TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
              SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    707 ATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 19-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
TOPOLOGY:
                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spSerTrpGlyGlnGlyThrThrLeuThrValSerSer 237
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                                                                                                                                           (415) 576-0200
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; MOLECULE TYPE: US-08-875-811-49

protein

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alignment_block:
US-08-487-283A-8 x US-08-875-811-49
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                                                                                                                      132
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spSerTrpGlyGlnGlyThrThrLeuThrValSerSer
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Ratio:
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3.938
82.114
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                                                          ....ThrProLeuTyrTyrPheA
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; NAME/KEY: Protein; LOCATION: 1..355; OTHER INFORMATION: US-08-875-811-64
                                                                                                                                                                                alignment_block:
US-08-487-283A-8 x US-08-875-811-64
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                                                                                                                                            Align seg 1/1 to: US-08-875-811-64
                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:

NAME: Faris, Susan K.

REGISTRATION NUMBER: 41,73

REFERENCE/DOCKET NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-03-
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
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APPLICATION NUMBER: WO P
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998
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ZIP: 94111-3834
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                          GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGA
                                                                                                                                                                                                                                                       Quality:
Ratio:
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Boque, Lluis
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21-FEB-1996
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                                                                                                                                              from: 1
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Gaps:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                            Sequence 45, Application US/08875811 Patent No. 6045793
                                                                                                                               GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
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                    COUNTRY: USA
ZIP: 94111-3834
                                                        CITY: San Francisco
STATE: California
                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
                                                                                                                                                                                                                                                                                                                                                                                                                CTATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCCGAATTGGTATTTTG 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTACAGTATACATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyThrLysLeuGluIleLys.....GlyGlyGlyGlySerGlyGlyGl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyIleTyrTyrCysLeuGlnTyrAspGluPheProTyrThrPheGlyGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACT 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGATCTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCC 406
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Center, Eight
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                                                                                              Crew LLP
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alignment_block: us-08-487-283a-8 \times us-08-875-811-45
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Percent Similarity:
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APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Faris, Susan K.

REGISTRATION NUMBER: 41,739

REFERENCE/DOCKET NUMBER: 015280-244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         233
                                                                           357
                                                                                                                  219
                                                                                                                                                      307 GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGG 356
                                                                                                                                                                                                                                  257 CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                  107 ACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 19-FEB-199
CLASSIFICATION: 435
407 AGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGC
                                                                                                                                                                                               202 lylleTyrTyrCysLeuGlnTyrAspGluPheProTyrThrPheGlyGly 218
                                                                                                                                                                                                                                                                                                                                                        169 AlaAsnArgLeuValAspGlyValProSerArgPheSerGlySerGlySe 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 GATATCCAGATGACCCAGTCCCCGTCCTCCTGTCCGCCTCTGTGGGCGA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                         TGGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCG 406
                                                                                                                  GCGACGAACCTGGCAGATGGAGTCCCCTTCTCGCTTCTCTGGATCCGGCTC
                                    yGlySerGlyGlyGlySerGluValGlnLeuGlnGlnSerGlyThrV
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FBRIS, SUSAN K
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: TWO CITY: San STATE: Cal
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrThrPheSerSerTyrTrpMetHisTrpIleLysGlnArgProGlyGl
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                 amino acid
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                                    358 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and Townsend and Crew LLP
                                                                                                                  (415) 576-0200
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; MOLECULE TYPE: US-08-875-811-51
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Quality:
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                                                                                                                       333 lTyrTyrCys.....
                                                                                                                                                                                                                                                                                                                                                                                                                              407 AGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGC 456
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ATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC 744
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Gaps:
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343 spSerTrpGlyGlnGlyThrThrLeuThrValSerSer

seq\_name:

/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:US-08-875-811-47

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; MOLECULE TYPE: US-08-875-811-47
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    Sequence 47, Applicati
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INFORMATION FOR SEQ ID NO:
                                                               137
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FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Recombinant Ribonuclease NUMBER OF SEQUENCES: 64
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                       GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGA
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Boque, Lluis
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21-FEB-1996
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Dianne L.
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                         APPLICANT: Newton, Dianue ...
APPLICANT: Newton, Dianue ...
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
APPLICANT: Wlodawer, Alexander
APPLICANT: NVENTION: Recombinant Ribonuclease Proteins
                                                                                                                                                                                             NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
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                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                 ZIP:
                                                                                                                                                                         CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATTATTGCGCGCGTTATTTTTTGGTTCTAGCCCGAATTGGTATTTTG 706
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    Application US/08875811
6045793

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                      Version
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CLASSIFICATION:

APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998

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alignment_block:
US-08-487-283A-8 x US-08-875-811-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60 FILING DATE: 21-FEB-1996 ATTORNEY/AGENT INFORMATION: NAME: Faris, Susan K.
                                                                                                                                                                                                                                          307
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457 TATATTTTTTCTAATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCA 506
                                                    274 alleuAlaArgProGlyAlaSerValLysMetSerCysLysAlaSerGly 290
                                                                                        407 AGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGC 456
                                                                                                                                                                                                  243 GlyThrLysLeuGluIleLys.....GlyGlyGlyGlySerGlyGlyGl 257
                                                                                                                                                                                                                                                                            226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 GATATCCAGATGACCCAGTCCCCGTCCTCCCTGTCCGCCTCTGTGGGCGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 41, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                   GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGG
                                                                                                                                                                                                                                                                                             CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGATCTGGTGGCGGCGCTCTCAAGTCCAACTGGTGCAATCCGGCGCCG 406
                                                                                                                                                                                                                                                                        lyIleTyrTyrCysLeuGlnTyrAspGluPheProTyrThrPheGlyGly 242
                                                                                                                                                                                                                                                                                                                                              GCGACGAACCTGGCAGATGGAGTCCCCTTCTCGCTTCTCTGGATCCGGCTC 206
                                                                                                                                                                                                                                                                                                                                                                                  CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTCG 256
                                                                                                                            Quality:
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19-FEB-1997
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3.938
82.114
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18,
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,054C
FILING DATE: 13-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,420
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Addiago, Sarah B.
RECICETATATION NUMBER: 34.470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                        TELEFAX: 310-445-9031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 SerThrAlaTyrMetGluLeuAsnSerLeuThrAsnGluAspSerAlaVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Expression Vectors Encoding Bispecific TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 spSerTrpGlyGlnGlyThrThrLeuThrValSerSer 379
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                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                          TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
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TOPOLOGY:
                 STRANDEDNESS:
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                                        amino acid
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11150 Santa Monica Blvd., Suite 400
                                                            302 amino acids
                                                                                                                            310-445-903
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Linsley, Peter S.
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                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0,
linear
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alignment_block:
US-08-487-283A-8 x US-08-121-054C-18
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seq_documentation_block:
                                     seq_name:
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90 rGlyThrAspTyrSerLeuThrIleAlaAsnLeuGlnProGluAspIleA 107
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57 snTrpTyrGlnGlnLysProAspGlyThrValLysLeuLeuIleTyrTyr 73
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                                                                        CACGGCCGTCTATTATTGCGCGCGCGTTATTTTTTGGTTCTAGCCCGAATT 697
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                                     /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-539-436-18
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3.871
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Gaps:
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alignment_block:
US-08-487-283A-8 x US-08-539-436-18
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APPLICATION NUMBER: US 08/121,054
FILING DATE: 13-SEP-1993
APPLICATION NUMBER: US 08/013,420
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
PRETISTRATION NUMBER: 34 470
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APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,436
FILLING DATE: 05-CCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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APPLICANT: Fell, Perry
                                                                   107 ACTGGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGT 156
157 GCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGGCTC 206
                                             57
                                                                                                                                    40 pArgValThrIleSerCysArgAlaSerGlnAspIleArgAsnTyrLeuA
                                                                                                                                                                                    57 TAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGGCGCGCTGA 106
                                                                                                                                                                                                                               24 AspIleGlnMetThrGlnThrThrSerSerLeuSerAlaSerLeuGlyAs
                                                                                                                                                                                                                                                          7 GATATCCAGATGACCCAGTCCCCGTCCCCTGTCCGCCTCTGTGGGGCGA
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CITY: Los Angeles
STATE: CA
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                           snTrpTyrGlnGlnLysProAspGlyThrValLysLeuLleuIleTyrTyr
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Linsley, Peter S.
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74	ThrSerArgLeuHisSerGlyValProSerArgPheSerGlySerGlySe 90	
207	CGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTTCG 256	
90	rGlyThrAspTyrSerLeuThrIleAlaAsnLeuGlnProGluAspIleA 107	
257	CTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAG 306	
107	laThrTyrPheCysGlnGlnGlyAsnThrLeuProTrpThrPheGlyGly 123	
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354	CGGTGGATCTGGTGGTGGCGGTTCTCAAGTCCCAACTGGTGCAAT 397	
140	yGlyGlySerGlyGlyGlyGlySerIleAspGluValGlnLeuGlnGlnS 157	
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548	GCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGAC 597	
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240	pSerAlaValTyrTyrCysAlaArgSerGlyTyrTyrGlyAspSerAspT 257	
869	GGTATTTTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGC 744	
257	rpTyrPheAspValTrpGlyAlaGlyThrThrCysThrValSerSer 272	

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: 9b_ba1:
2: 9b_ba3:
3: 9b_ba3:
4: 9b_in1:
5: 9b_om:
6: 9b in3:
6: 9b in3:
7: 9b_p
11: 9b_
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

44 W B V B	Result No.
482.8 478.2 476 476 476 476 476 476 476	Score
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1418 1599 9209 9209 9209 9209 9209 18986 18986	ength D
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                  HEPAH 1599 bp mRNA PRI 08-OCT-199
(hybridoma H210) anti-hepatitis A IgG variable region,
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CCCAAATCTTGTGACAAAACTCACACAT 748
                                                                      ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGTTGAG
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CCCAAATCTTGTGACAAAACTCACACAT
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KEYKCKVSNKALEAPIEKTISKAKGQPREPQVYTLDPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HHNYTQKSLSLSFGK*
a 445 c 374 g 260 t
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93367243
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J. Immunol. 151 (5), 2829-2838 (1993)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1599)
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Homo sapiens cDNA to mRNA.
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1463. 1599
/note="putative"
1566. 1571
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a 526 c .441 g 27:
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182. 196
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473. .1462
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386. .439
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239. .289
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VFSCSVMHEALHNHYTQKSLSLSPGK"
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239. .289
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                                                                  human B lymphocyte restricted diffe of B cell lymphoma Patent: US 5736137-A 3 07-APR-1998;
                                                                                            Rastetter, W.H.
Therapeutic application of chimeric and radiolabeled antibodies to
                                                                                                                                                                                                                                    Sequence 3 from AR000007
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Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and
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(bases 1 to 9209)
Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rastetter,W.H.
Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma
Patent: US 5776456-A 2 07-JUL-1998;
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AR051652
Sequence
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Location/Qualifiers
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Reff,M.R., Barnett,R.Spence and McLachlan,K.Retta.
Method for integrating genes at specific sites in mammalian via homologous recombination and vectors for accomplishing t Patent: US 5998144-A 2 07-DEC-1999;
Location/Qualifiers
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US 5998144
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No. 8.2e-103;
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                                                                                                                    GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATATACC
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                             GAGTTGAGGAGCCTCAGGTCTGCAGACACGGCTGTTTATTATTGTGCGAGAGTGGGGCCCA
                                                                   GCGAAGTTCCAGGACAGAGTCACCTTTACCGCGGACACATCCGCGAACACAGCCTACATG
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Sequence
AR038306
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Burton,D.R., Barbas,C.F. and I
-CGTTATTTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACC
                                                                                                                                                                                                                                                                                                                                                                  Patent:
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1109 c 864 g
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1. .3282
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patent US
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Pred. No. 1.2e-100;
0; Mismatches 141;
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Best Local Similarity 78.7
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                                    TGTAAAGCTAGCGGCTATATTTTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCC
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GCGAAGTTCCAGGACAGAGTCACCTTTACCGCGGACACATCCGCGAACACAGCCTACATG
                                                                         TGTCAGGCTTCTGGATACAGATTCAGTAACTTTGTTATTCATTGGGTGCGCCCAGGCCCCC
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Sequence
AR038320
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1 (bases 1 to 3282)
Burton, D.R., Barbas,
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GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACC
                                    TGTAAAGCTAGCGGCTATATTTTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCC
                                                                     GTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCC
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                           TGTCAGGCTTCTGGATACAGATTCAGTAACTTTGTTATTCATTGGGTGCGCCAGGCCCCC
                                                            GTTCAGCTGGTTCAGTCCGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCT
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Sequence
158595
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Burton,D.R., Barbas,C.F. and Lerner,R.A.
Human neutralizing monoclonal antibodies
                                                                                                                                                                                                                         Patent:
                                                                                                                                                                                                                                                                            Unknown.
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1109 c 864 g
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BASE COUNT
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Best Local Similarity 78.7%;
Matches 577; Conservative
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                                          ATGGAATGGAGCTGGGTCTTTCTTCTTCCTGTCAGTAACTACAGGTGTCCACTCCCAG
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                                                                                                                                                                                                                                                                                                                  Sequence
I58609
                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 3282)

Burton,D.R., Barbas,C.F. and
Human neutralizing monoclonal
                                                                                                                                                                                                   Patent: US 5652138-A 169 29-JUL-1997;
                                                                                                                                                                                                                virus
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Pred. No. 1.2e-100;
0; Mismatches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
AR038307
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Burton,D.R., Barbas,C.F. and Lerner,R.A.
Human neutralizing monoclonal antibodies
                                                                                                                                Patent:
                                                                                                                                                                                   Unclassified.
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                                        Similarity
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                              Score 467.4; DB 9;
Pred. No. 9.4e-101;
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Burton,D.R., Barbas,C.F. and Lerner,R.A.
Human neutralizing monoclonal antibodies
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1 (bases 1 to 13254)

Burton,D.R., Barbas,C.F. and Lerner,R.A.

Human neutralizing monoclonal antibodies
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Unpublished (1999)
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can
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Plate: LLCM1205 row: 1 column: 12
High quality sequence stop: 759.
Location/Qualifiers
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Pred. No. 3.5e-106;
0; Mismatches 150;
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                                                                             TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGCAGTTGCTATATATGGTATGATGGA 125
                                                                                                    TGGGTGCGTCAGGCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCT 222
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AGTARTCAATACTACACAGACTCCGTGAAGGGCCGATTCACCGTCTCAAGAGACAATGTT 185
                                    GGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCG 282
                                                                                                                                                              GCGTCCGAGAGACTCTCCTGTGCAGCCTCTGGATTCATCTTCAAAAACTATGGCATGAAC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF342599 783 bp mRN 602013731F1 NCI_CGAP_Brn64 5', mRNA sequence.
BF342599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 744.
Location/Qualifiers
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Plate: LLAM9411 row: m column: 08
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1 (bases 1 to 783)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn64"
/clone_lib="NCI_CGAP_Brn64"
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/tissue_type="glioblastcma with EGFR amplification"
/lab_host="PM108 (Tl phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Life
Technologies. Note: this is a NCI_CGAP Library."
85 a 235 c 209 g 154 t
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76.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG397867 860 bp
602438967F1 NIH_MGC_48
mRNA sequence.
BG397867
                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1281 row: f column: 17
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Clone distribution: MGC clone distribution information
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                                                                                                                                   quality sequence stop: 846
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/db_xref="taxon:9606"
/clone="IMAGE:4565008"
/clone=lib="NIH_MCC_48"
/clone_lib="NIH_MCC_48"
/tissue_type="primary B-cells from tytissue_type="primary B-cells from tytissue_type="primary B-cells from type="bhilde"/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Lin Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Pred. No. 2.1e-102;
0; Mismatches 179; Indels
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CGCGCGTTATTTTTTTGG-----TTCTAGCCCGAATTGGTATTTTGATGTT
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                                                                                                                     GGTGGCCAAGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 775)
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National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
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/db_xref="taxon:9606"
/clone="IMAGE:4565676"
/clone_lib="NIH_MCC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
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              ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA 60
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                                                                    580;
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BG397847
BG397847.1 GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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602438939F1 NIH_MGC_48
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                Similarity
                                                                52.5%;
nilarity 76.3%;
Conservative
                                                                                                                                                                      200
                                                                                                                                                                 /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by Oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH_MGC Library."

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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_48"
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Pred. No. 1e-100;
0; Mismatches 159;
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           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
That Library Proparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                    C-CTCAGCTCCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT
                                                                                                                                                                                                                                                                                                                                                                                                          CGAGCGCCTCCAACGAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCCAAGAGCACCT
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  AGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACCCAAGGTGGACAAGAAGTTG
                                                 GAGCTGAGGAGCCTGAGATCTGACGACACGG-CGTCTATTACTGTGCGAGGGCATATTGT
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                                                                                                      CCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC
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/clone_lib="NAH_MGC_48"
/clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (post)
/lab_host="DH10B (post)
/lab_host="DH10B (phage-resistant)"
/lab_host="DH
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/db_xref="taxon:9606"
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                                         ATGGCGCCAGTACATACTACGCAGACTCCGTGAAGGGCCGCTTCACCATCTCCAGAGACA 181
                                                                                                                                             CTGGGGGGTCCCTGAGACTCTCCTGTGCGGCCTCTGGGTTCATCTTTGACAAACATGGCA 61
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                                                                                                                          TGACCTGGGTCCGCCAGGCCCCAGGGAAGGGGCTGGAGTGGGTCTCAGGGATTAGTGGTA 121
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                                                                                                                                                                                                                                                                                     503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M
cDNA Library Preparation: Ling Hong/R
cDNA Library Arrayed by: The I.M.A.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 796)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602439885F1 NIH_MGC_48
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                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note: ECORI; CDNA made by oligo-dT priming.
/note: Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GCACGA6(G). Size-selected >500bp for average insert size 1.8kb Library.constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
/note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4566236"
/clone_lib="NIH_MGC_48"
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                                                                                                                                                                                                                                                                                                        50.9%;
75.9%;
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.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                        DB 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTACTGTGCGAAAGAACTCTTGCCGGTGACTTCTGTGATTGTTGTGGAGGGCGCTATGG
                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG397667
BG397667.1 GI:
                                                                                                                                                                                                                                          1 (bases 1 to 841)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 841)
                                                                                                                                                                                                                                                                                                                                                            BG397667 841 bp
602438719F1 NIH_MGC_48
                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                  Unpublished (1999
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               662
/Clone="IMAGE:4564973"
/Clone_lib="NIH_MGC_48"
/Clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                          Chordata;
Primates;
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IMAGE:4564973
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RESULT BF663151 LOCUS

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DEFINITION

BF663151 864 bp 602145073F1 NIH\_MGC\_48 mRNA sequence.

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Pred. No. 1.2e-93;
0; Mismatches 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 864)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Clone distribution: MGC clone distribution information can
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//Clone_11b="NIH_MGC_48"
//Clone_11b="Primary B-cells from tonsils (cell line)"
//tissue_type="primary B-cells from tonsils (cell line)"
//lab_host="DH10B (phage-resistant)"
//lab_host="DH10B (phage-resistant)"
//note="Oygan: B-cells; Vector: pOTB7; Site_1: XhoI;
//note="Oygan: p
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/db_xref="taxon:9606"
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Pred. No. 1.3e-92;
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BF663258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                   212
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                                                                                                             /clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_most="DH10B (phage-resistant)"
/lab_most="DH10B (phage-resistant)"; Site_1: XhoI;
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
12 a 297 c 296 g 177 t 1 others
                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4297818"
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/db_xref="taxon:9606"
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Primates;
Score 364; DB Pred. No. 2.6e 0; Mismatches
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DB 151;
2.6e-92;
les 195;
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Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y.,
H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Che
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., 2
,G., Hu,R., Chen,J., Chen,Z. and Han;Z.
Homo sapiens cDNA ADC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong
201203, P. R. China
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 653)
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ACCESSION VERSION KEYWORDS SOURCE

EST. human.

DEFINITION

AW403676 489 bp mRNA UI-HF-BKO-abh-c-03-0-UI.rl NIH\_MGC\_36 IMAGE:3056237 5', mRNA sequence. AW403676.1 GI:6922685

Homo

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16-FEB-2000 cDNA clone

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Fax: 86-21-50801922
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lone is available at Cl
Location/Qualifiers
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/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-);
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/db_xref="taxon:9606"
/clone="ADCAXE01"
/clone_lib="ADC"
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Pred. No. 4.5e-92;
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                                                                                                                                                                                                                                                                                                                                                                   176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 CCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCC 371
  416
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                                                                                                                                                                                                       AGGCGCCCTGACCAGCGGCGTGCACACCCTTCCCCGGCTGTCCTACAGTCCTCAGGACTCTA 611
                                                                                                                                                                                                                                                                                             GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGCGCCTCCAC 431
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTG
                                                                                                                                                                              AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/db_xref="taxon:966"
/clone="IMAGE:3056237"
/clone_lib="NIH_MGC_36"
/tissue_type="1ymph"
/cell_type="germinal center B
/cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DHIOB (LTI)"
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Lou
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

159 c 126 g 88 t
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Pred. No. 8.1e-92;
0; Mismatches 65
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                                                                                                                                                                   TGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCC 180
                                                                                                                                                                                                                                                                                                                                                                                        ATGGACTGGACCTGGAGGGTCTTCTGCTTGTTGGCTGTAGCTCCAGGTGCTCACTCCCAG 100
GGACAAGGGCTTGAATACATGGGAATAATCAACCCTAGTAGCGGTAGTCCAAACTACGCA 280
                                                                                                                                                                                                                                                             GTGCAGCTGGTGCAGTCTGGGGGCTGAGGTGAGGAAGCCTGGGGGCCTCAGTGAAGGTTTCC
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602144936F1 NIH_MGC_48 Homo sapiens cDNA
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Tissue Procurement: Louis M. Staudt, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF663033.1 GI:11936928 EST.
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BF663033
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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Plate: LLCM1180 row: h column: 10
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Similarity 74.2%;
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//db_xref="taxon:9606"
//clone="IMAGE:4308537"
//clone=lib="NIH_MGC_48"
//clone=lib="NIH_MGC_48"
//clone=type="primary B-cells from tonsils (cell line)"
//tissue_type="primary B-cells from tonsils (c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 360.8; DB 151; Length 936; Pred. No. 2.1e-91;
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BF128792
BF128792.1 GI:
EST.
                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM83 row: p column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF128792 779 bp
601811172F1 NIH_MGC_48
                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                             quality sequence stop:
Location/Qualifiers
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Li
                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4054144"
/clone_lib="NIH_MGC_48"
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DEFINITION ACCESSION RESULT 1 AW606355 LOCUS

AW606355 669 bp mRNA QV0-HT0366-280100-088-b12 HT0366 AW606355 AW606355.1 GI:7311096 EST.

Homo

sapiens

CDNA,

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sequence

SOURCE KEYWORDS VERSION 닭 δõ 밁 δõ 멍 Ş В Ş 밁 δÃ 밁 δÃ 밁

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498 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 557	438 CCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT 497	378 GTATTITGATGITTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGCGCCTCCACCAAGGG 437	340 TATTGCGCGCGTATTTTTTTGGTTCTAGCCCGAATTG 377	280 TCGACTAGTACAATGGAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTAT 339	220 TCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACT 279	160 CAATGGGTGAGGCCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGC 219	100 GGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGATT 159	Query Match 47.8%; Score 358.4; DB 118; Length 669; Best Local Similarity 73.8%; Pred. No. 9.1e-91; Matches 493; Conservative 0; Mismatches 151; Indels 24; Gaps 2;	Brazil Tel: +55-11-2704 Fax: +55-11-2704 Fax: +55-11-2707 Email: asimpson@ This sequence wa Project This en (http://www.ludw 280100-088-b124t Seq primer: puc High quality seq High quality seq High quality seq /organi 1 .669 /organi /dev_st /note-* /dev-st /note-* /dev-st /note-* /derived No.196 profile tissue low str NT 160 a 191	ISM . RS

Search completed: July 20, 2001, 01:57:51 Job time: 4179 sec

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1: /SIDS1/gcgdata*
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## ALIGNMENTS

02-APR-1996 (first entry)

AAT08484;

AAT08484 standard; DNA;

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Humanised 5G1.1 VH + IGHRLC DNA.

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Best Local Similarity 100.
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                            A DNA construct (AAT08487) codes for a humanised CDR-grafted light chain, designated 5G1.1 VL + IGHRLD (AAR77615), which incl. CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (AAT08484) coding for a humanised Fd (AAR77611) into vector APEX-3P (AAT08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                              Claim
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humanised antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evans MJ,
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                     Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
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                                                                        ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAAGTTGAG
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Pred. No. 4.9e-126;
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disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mini the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence encodes a humanised anti-Fas antibody HFE7A heavy chain construct HHH type which is described in the method of the invention.
                                                                                                                                                                                                                                                                             immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antirhertility, neuroprotective, antirheumatic, nephrotropic, antirhertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the ras/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's antirious or disease, Sjorgen's syndrome, pernicious or hypoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyrominetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; enemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the sell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention
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30-SEP-1998;
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1999;
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98JP-0276882.
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diagnosis; inflammatory disorder;
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                                                                      GAGCTCTCCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCGCGTTATTTTTT
                                                                                                                                GAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATG
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cgctacaatggtgactggttcttcgacgtctggggtcaaggaaccctggtcaccgtctcc
                           GGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCG
                                                        çagatgaacagcctgcgtgctgaggacactgccgtctattactgtgcaagaggggattat
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(MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 (664.2.5V11N35A light chain; and amino acids 24-253 of the humanized anti-IL-8 (664.2.5V11N35A heavy chain. The anti-IL-8 MAbs and fragments can be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory disorders e.g. adult respiratory distress syndrome. Nuclei
                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule encodes a polypeptide which is an anti-interleukin-8 monoclonal antibody or antibody fragment the production of anti-interleukin-8 monoclonal antibodies or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disorder; adult respiratory distress syndrome; affinity purification; ss.
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                                                                                                                                                                                                           invention relates to an anti-interleukin-8 (IL-8) monoclonal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanized anti-interleukin 8 monoclonal antibody variant useful for treating inflammatory disorders, such as adult respiratory distress syndrome, hypovolemic shock and ulcerative colitis -
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                  GGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCTGGTCACTGTCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEE/A, monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE/A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease;
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rejection; therapy; ds.
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ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAA 60

Query Match Best Local S Matches 585

Similarity

65.9%; 81.5%;

Conservative

0

Score 494; DB 19; Pred. No. 8.7e-110; 0; Mismatches 130;

Length 2071;

Gaps

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77777
                                 Chain (see AAM83037) of murine anti-human Fas monoclonal antibody
CC Chain (see AAM83037) of murine anti-human Fas monoclonal antibody
CF PERM amplification (see AAV70115-17), and includes humanising R44G
CC and A76T amino acid substitutions. Host cell Escherichia coli
CF pgHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion
CF fragment of the humanised HV type HFE7A heavy chain and DNA
CF producing human IgG1 constant region, and is deposited as
CF PERM BP-6273 (claimed). The invention provides methods for
CF producing humanised antibodies by culturing host cells. Humanised
CF producing humanised antibodies by culturing host cells. Humanised
CF producing humanised antibodies by culturing host cells. Humanised
CF producing apoptosis in abnormal cells expressing Fas, and of
CF inhibiting Fas-induced apoptosis in normal cells. The humanised
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01-APR-1997;
25-JUN-1997;
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Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;
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used to evaluate drugs in animal models and to treat Fas-associated
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Nobufusa S, Shin Y,
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97JP-0082953.
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Y, Tohru
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  Preventive or treating
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DB; AAB14779.
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in the Fas/Fas ligand system e.g. autoimmune anti-Fas antibody – \ensuremath{^{\circ}}
                                                                                Example
                                                                                22;
                                                                                Page 106-108;
                                                                                               diseases,
                                                                                               contains
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or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its (not complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autolimune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, and organ graft rejection. Sequences AAA72146, AAA72159 and AAA72184 represent DNA encoding the heavy chains (or fragments thereof) of various humanised HFE7A-derived anti-Fas antibodies. invention relates 6 compositions for the prevention or treatment

in

Sequence 2071 BP; 460 Α, 685 C; 561 G; 365 T; 0 other;

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cc immunomodulatory, dermatological, immunosuppressive, thyromimetic, cardiant and hepatropic activity. (I) induce cardiant and hepatropic activity. (I) induce capoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent cdiseases associated with the Fas/Fas ligand system, especially systemic lipus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's clisease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyrominetic, anti-fras; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; slepatotropic; humanized; apoptosis; systemic lupus erythematosus; sjorgen; syndrome; anemia; Addison; s disease; scleroderma; sterility; syotrome; crohn; disease; sterility; myasthenia gravis; multiple sclerosis; Basedow; sdisease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1998;
30-SEP-1998;
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                                                                                                                                     AAA11646 standard;
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81.5%;
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Fas; antibody; human; anti-inflammatory; anti-anemic; anti-allergic; anti-arthritic; antiviral; immunomodula

thyromimetic;

immunomodulatory; car
imetic; antirheumatic;

antidiabetic;

08-AUG-2000

(first entry)

anti-Fas

designed

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CC immunomodulatory, dermatological, immunosuppressive, thyronimetic, cardiant and hepatropic activity. (I) induce cantirheumatic, nephrotropic, antiinfertility, neuroprotective, cantirheumatic, nephrotropic, antiinfertility, neuroprotective, cc antirheumatic, nephrotropic, antiinfertility, neuroprotective, cc antirheumatic, nephrotropic, antiinfertility, neuroprotective, cc antirheumatic to cell surface Fas or inhibit it by competitive cc inhibition of ligand binding. (I) are used to treat and/or prevent cc diseases associated with the Fas/Fas ligand system, especially systemic cc lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft cc versus host disease, Sjorgen's syndrome, pernicious or hypoplastic cc anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's cc disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cc multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin cc dependent disbetes mellitus, allergy, arteriosclerosis, myocarditis, cc disease, allergy, arteriosclerosis, myocarditis, cc disease, allergy, arteriosclerosis, myocarditis, cc disease, allergy, arteriosclerosis, myocarditis, cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cc inhibit apoptosis in normal cells but selectively induce it in abnormal cells in the mathody response. This sequence encodes c humanised anti-Fas antibody heavy chain construct designated Heu 3 whi
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabet anti-allergic; anti-arthritic; antiviral; immunomodulatory; card dermatological; immunosuppressive; thyromimetic; antirheumatic;
                          New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induced cells with abnormal Fas-Fas ligand systems
                                                                                                                                 Serizawa
                                                                                                                                                                                            30-SEP-1998;
30-SEP-1998;
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Claim 34; Page 172-174; 263pp; English

apoptosis

selectively

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cc antirheumatic, nephrotropic, antiinfertility, neuroprotective, cardiant and hepatropic activity. (I) induce capoptosis by binding to cell surface Fas or inhibit it by competitive clinibition of ligand binding. (I) are used to treat and/or prevent cd diseases associated with the Fas/Fas ligand system, especially systemic culture erythematosus, Hashimoto disease, Indunatodia arthritis, graft cursus host disease, Sorgen's syndrome, pernicious or hypoplastic canemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's cdisease, autoimmune hemolytic anemia, sterility, myasthenia gravis, cultiple sclerosis, Basedow's disease, thrombopenia purpura, insulin cdependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic clinibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence encodes a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention.
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Sequence 2073 BP; 464 A; 685 C; 558 G; 366 T; 0 other;

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Best Local Similarity 81.2
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 TCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
                             gggggcacagcggccctgggctgcctggtcaaggactacttccccgaaccggtgacggtg
                                              GGGGGCACAGCGGCCCTGGGCTGGCCTGGTCAAGGACTACTTCCCCCGAACCGGTGACGGTG
                                                                                                                        AGCGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCT
                                                                                                                                                    gactatagtaacaactggtacttcgatgtctggggccaaggtacactggtcaccgtctcc
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81.2%;
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Pred. No. 5.
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Mismatches 132; Indels
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This is the DNA sequence of vector plasmid p6G4V11N35A.choSD.9 encoding a humanised 6G4V11N35A IgG (see ANA69316) containing complementarity determining regions of murine anti-interleukin-8 (IL-8) monoclonal antibody (MAD) 6G5.2.5 (see ANA69309-10) in a human template. The plasmid has a pSVI backbone. Humanised anti-IL-8 MADs (see ANA69301-04) are described for use in diagnostic applications and in the treatment of inflammatory disorders. The invention provides conjugates of an antibody fragment and a polymer, such as PEG, that have improved half-life, mean residence time, and/or clearance rate. The conjugates can be used for immune

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                                                                                                                                                                                                                                                                                                                                  non-proteinaceous polymer molecules, particularly polyethyloglycol, for improving the residence time in the circulation
                                                                                                                                                                                                                                                                                                                                                             New conjugates of antibody fragments - having covalently attached non-proteinaceous polymer molecules, particularly polyethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-1998;
21-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody; chimeric antibody; monoclonal antibody; human; Fab; interleukin-8; inflammation; immunotherapy; pso;
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0; Mismatches 161; Indels
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1: /cgn2_6/ptodata/2

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    324599 seqs, 94655562 residues
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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    DB
3 US-09-027-449-68
3 US-09-026-985-68
3 US-09-027-449-69
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3 US-09-027-449-61
3 US-08-08-04-61
3 US-08-08-08-98-5-61
3 US-08-08-149-090-3
3 US-08-149-090-3
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3 US-08-276-852-159
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GENERAL INFORMATION: APPLICANT: GONZALEZ, TANI APPLICANT: GONZALEZ, TANI APPLICANT: GONZALEZ, TANI APPLICANT: LEONG, Steven APPLICANT: LEONG ANDRESSE: GENERECH, I STREET: 1 DNA WAY CITY: SOUTH SAN FRANCIS SOUNTRY: USA ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch. COMPUTER: IBM PC compat OPERATING SYSTEM: PC-NO SOFTWARE: WinPatin (Gen CURRENT APPLICATION NUMBER: US, FILING DATE: 20-Feb-199 PRIOR APPLICATION NUMBER: 60, FILING DATE: 22-Jan-199 PRIOR APPLICATION NUMBER: 34 APPLICATION NUMBER: 36 APPL	44444444466666666666666666666666666666
149-68 149-68 1APPLICATION UNDEER: NG DATE: 20-Feb- ENG DATE: 20-Feb- ENG DATE: 20-Feb- ENG DATE: 20-Feb- ENG DATE: 21-Feb- ENG DATE: 31-Feb- ENG DATE: 31-F	62.3 62.3 62.3 62.3 62.3 61.7 61.7 61.7 61.3 61.3 61.3 61.3 61.3 61.3
Sonzalez, Tania R. Leong, Steven R. Yesta, Leonard G. NATION: Antibody Fra NATION: Humanized An DUENCES: 72 E ADDRESS: Genentech, Inc. DNA Way In San Francisco Lifornia 3.5 inch, 1.44 Mb IBM PC compatible PC-DOS/MS-DO Winfath PC-DOS/MS-DO WINGBER: US/09/027, 11 NUMBER: 60/074,330 12 - Feb-1998 17 INFORMATION: Richard B. Richard B. RICHARD WINGBER: 34,659 WOCKET NUMBER: 91085 TION INFORMATION: 650/225-5530 SO/952-9881 SEQ ID NO: 68: Linear	13254 13254 13254 13254 13254 13254 13254 2143 6550 1655 762 762 762 762 762 762 762 762 762 762
US/09027449 Tania R. yeen R. onard G. ntibody Fra umanized An 72 h, Inc. ncisco ch, 1.44 Mb mpatible ch, 1.60/074, 330 -1998 :: 60/074, 330 -1998 :: 60/038,664 -1997 TION: B. B. G.	1 US-1 1 US-1 1 US-1 1 US-1 1 US-1 3 US-3 3 US-3 3 US-3 1 US-1 1 US-1 1 US-1 2 US-3 3 US-3 3 US-3 3 US-3 3 US-3 3 US-3 3 US-3 3 US-3 1
Tania R. even R. even R. eonard G. Antibody Fragment- Humanized Anti-IL- 72 S: ch, Inc. ancisco  PC-DOS/MS-DOS (Genentech) ATA: US/09/027,449 b-1998 5 A: 60/074,330 n-1998 A: 60/038,664 b-1997 ATION: d B. 460/038,664 b-1997 ASTION: d B. 610/038,664 b-1997 ASTION: d B. 610/038,664 b-1997 ASTION: d B. 610/038,664 b-1998 A: 610/038,664 b-1997 ASTION: d B. 610/038,664 b-1998 ASTION:	8-08-899-575 8-08-899-575 8-08-899-575 8-08-899-575 8-08-99-575 8-09-097-309 8-09-027-712 8-09-049-672 8-09-049-672 8-09-049-672 8-09-049-672 8-09-049-672 8-09-049-672 8-09-049-672 8-09-049-673 8-08-398-611 8-08-398-611 8-08-398-611 8-08-398-611 8-08-398-633 8-09-027-449 8-08-804-444 8-09-027-449 8-08-804-444 8-09-026-985 8-09-026-985
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	170, App 156, App 170, App 170, App 156, App)1 5, App)1 21, App)1 21, App)1 57, App)1 57, App) 57, App) 57, App) 43, App) 43, App) 43, App) 43, App) 43, App) 43, App) 44, App)

Query Match

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Score 495.2;

DB 3;

Length 8120;

78.98;

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us-09-026-985-68
                                                                                                                                                                                             ; Sequence 68, Application, Patent No. 6133426; GENERAL INFORMATION: APPLICANT: Gonzale; APPLICANT: Leong, APPLICANT: Presta,
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                                                                                                       APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
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                    ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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0; Mismatches 158;
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Best Local S
Matches 590
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
COMPUTER: IBM PC COM
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TOPOLOGY: Lir
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GGGGGCACAGCGGCCTGGGCTGGTCAAGGACTACTTCCCCCGAACCGGTGACGGTG
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                                                                  TCGTGGAACTCAGGCGCCTGACCAGCGGCGTGCCACCTTCCCGGCTGTCCTACAGTCC
                                                                                                   TCGTGGAACTCAGGCGCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
                                                                                                                                    GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG
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                                                                                 Nucleic Acid
DEDNESS: Single
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78.9%;
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Pred. No. 1.8e-119;
0; Mismatches 158;
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Best Local Similarity
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APPLICANT: Gonzal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/0:
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/074,330 FILING DATE: 22-Jan-1998 PRIOR APPLICATION DATA:
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1966
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CURRENT APPLICATION DATA:
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141 TTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGAT
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APPLICANT: Gonzal
                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                      APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodie
             ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
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                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                         FILING DATE: 2
CLASSIFICATION:
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NAME: Love, Richard REGISTRATION NUMBER:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
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                                                              TCACACAT 790
                                                                                                                            TCACAAGCCCAGCAACACCAAGGTGGACAAGAAGTTGAGCCCAAATCTTGTGACAAAAC 740
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Nucleic Acid
DEDNESS: Single
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79.4%;
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Pred. No. 6.7e-118;
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Sequence 59,

Application US/09027449

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; GENERAL INFORMATION:
; APPLICANT: Gonzale:
APPLICANT: Leong, (
APPLICANT: Presta,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
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TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
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FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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363
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STRANDEDNESS: Single
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CITY: South San Francisco
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Local Similarity 79.4%;
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               GGAGGACACGGCCGTCTATTATTGCGCGCGTTATTTTTTTGGTTCTAGCCCGAATTGGTA
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                                                                      CACTTTATCTCGCGACAACTCCAAAAACACAGCATACCTGCAGATGAACAGCCTGCGTGC
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                                                                                                                                                                                 GGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGT
                                                                                                        TACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCTCCAGCCTGCGATC
                                                                                                                                               TGGATATTGATCCTTCCAATGGTGAAACTACGTATAATCAAAAGTTCAAGGGCCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 488; DB 3; Length 927; Pred. No. 7e-118;
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Pred. No.

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US-08-804-444A-59
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                                                                                                            APPLICATION UMBER: US/08/804,444A
APPLICATION UMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 650/225-5530
                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-TL-8 Monoclonal Antibodies
                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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                       TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                           CITY: South San
STATE: Californ:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                        927 base pairs
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                Linear
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                                                                                                                                                                                                                                                                                                                                                                                         Francisco
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Query Match

65.1%;

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                                                                                                                                Sequence 59, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
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                                                                                                   APPLICANT: Gonzalez, Tania R. APPLICANT: Leong, Steven R. APPLICANT: Presta, Leonard G. TITLE OF INVENTION: Antibody E TITLE OF INVENTION: Humanized
                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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             CITY: South San Francisco
STATE: California
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COUNTRY:
                                           STREET:
                                                         ADDRESSEE:
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                                           1 DNA Way
                                                         Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
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CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEO ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 578
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APPLICATION NUMBER: US,
FILING DATE: 20-Feb-199
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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CAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA
                                                                                                                                               TTTTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGGGCCCTCCACCAAGGGCCC
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                                                                       GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAG
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                                                                                                         GACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAG
                                                                                                                                                                                                                                                                                             CTTCGACGTCTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCGGCCTCCACCAAGGGCCCC
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Pred. No. 7e-118;
0; Mismatches 15
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US-09-027-449-61
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Matches 578
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APPLICANT: Gonzal
                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               TYPE: Nucleic Acid
STRANDEDNESS: Single
TOOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/03
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 6563 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                 1341 CGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTC
                                                                                                                1281 TATGTTCGTTTTTTCTATTGCTACAAACGCGTACGCTGAGGTTCAGCTAGTGCAGTCTGG
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                   141
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783 TCACACAT 790
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/0 FILING DATE: 22-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2
CLASSIFICATION:
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STATE: California
                                                                                                                                                                            Local Similarity
nes 578; Conserv
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TTTTTCTAATTATTGGATTCAATGGGTGCGTCAGGCCCCGGGCAGGCCTGGAATGGAT
                                                                                                                                             TCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAAGTCCAACTGGTGCAATCCGG
                                                                               CGCCGAGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCCTGTAAAGCTAGCGGCTATAT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-Feb-1998
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                                                                                                                                                                           Score 488; DB 3;
Pred. No. 1.2e-117;
0; Mismatches 150;
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US-08-804-444A-61
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                                                                                                                                                                                                                                    APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                  COMPUTER READABLE FORM:
MEDIOM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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                        ATTORNEY/AGENT INFORMATION:
                                                                                         CURRENT APPLICATION DATA:
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                                               APPLICATION NUMBER: US/0
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
                                                                                                                                                                                             CITY: South San FI
STATE: California
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
            NAME: Love, Richard B. REGISTRATION NUMBER: 3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTTTATCTCGCGACAACTCCAAAAACACAGCATACCTGCAGATGAACAGCCTGCGTGC
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Best Local S
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: Sing
TOPOLOGY: Linear
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Pred. No. 1.2e-117;
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US-09-026-985-61 ; Sequence 61, Application US/09026985 ; Patent No. 6133426

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CEC'S base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 TCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCACTCCCAAGTCCAACTGGTGCAATCCGG 80
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Local Similarity 79.48;
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ATCGGTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
                                                                                   TTTTGATGTTTTGGGGTCAAGGAACCCTGGTCACTGTCTCGAGCGCCTCCACCAAGGGCCC 440
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DEDNESS: Single
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Pred. No. 1.2e-117;
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US-08-378-939-9
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                                                                                                                                                                                                                                                  TELEFAX: (202) 783-bu INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PRODUCTION OF NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                     FEATURE
                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                          FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WASHINGTON STATE: D. C.
                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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; FEATURE:
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US-08-378-939-9
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US-08-149-099C-3
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                                                              Sequence 3, Application US/08149099C Patent No. 5736137
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Best Local Similarity
                                                    GENERAL INFORMATION:
APPLICANT:
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APPLICANT:
APPLICANT:
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LEONARD, John E. NEWMAN, Roland A. REFF, Mitchell E.
                             HANNA, Nabil
                                          ANDERSON, Darrell R.
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Pred. No. 2.9e-115;
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Best Local Similarity
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 03-NOV-199:
CLASSIFICATION: 424
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MOLECULE TYPE: DNA
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TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   2521
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                                                                                                                                                                                                                            181
                                                                        301
 361
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REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States ZIP: 22313-1404
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                        GAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATG 300
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GGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTCG
                                                                                                               CAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATG
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O. Box 1404
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Pred. No. 1.8e-114;
0; Mismatches 160;
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                                                APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY_AGENT INFORMATION:
NAME: Teskin, Robin L.
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APPLICANT:
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutle
TITLE OF INVENTION: Radiolabeled
TITLE OF INVENTION: Differentiat
TITLE OF INVENTION: Lymphoma
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CORRESPONDENCE ADDRESS:
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ZIP: 22314
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                                              Teskin, Robin L.
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Best Local S
Matches 585
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STRANDEDNESS: single
TOPOLOGY: circnlar
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTGCTACGCGTGTCCTGTCCCAG 2460
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                                                            ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAG
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Pred. No. 1.8e-114;
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US-08-478-967A-3

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Best Local (
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/478,967A
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APPLICANT: NEWMAN, Roland A.
APPLICANT: REFF, Mitchell E.
APPLICANT: RASTETTER, William H.
TITLE OF INVENTION: THERAPBUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
                                                                                                                                                          2461
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ZIP: 223
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CITY: Alexandria
STATE: Virginia
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                       1 ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGGGTCCACTCCCAA 60
                    GGGCAGGGCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACC 240
                                                                                                                                                                              GTCCAACTGGTGCAATCCGGCGCGAGGTCAAGAAGCCAGGGGCCTCAGTCAAAGTGTCC 120
GGTCGGGGCCTGGAATGGAGTTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAAT 2640
                                                                           TGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGACACCT 2580
                                                                                                   TGTAAAGCTAGCGGCTATATTTTTCTAATTAGTTGGATTCAATGGGTGCGTCAGGCCCCC 180
                                                                                                                                                          GTACAACTGCAGCAGCCTGGGGCTGAGCTGAAGCCTGGGGCCTCAGTGAAGATGTCC 2520
                                                                                                                                                                                                                                   ATGGGTTGGAGCCTCATCTTGCTCTTTCTTGTCGCTGTTGCTACGCGTGTCCTGTCCCAG 2460
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Pred. No. 1.8e-114;
0; Mismatches 160;
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US-08-819-866-2
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        COUNTRY: United States
ZIP: 2313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/819,866
FILING DATE: 14-MAR-1997
CILASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION UNMBER: 012712-35
REFERENCE/DOCKET NUMBER: 012712-35
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2641 CAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATG
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CITY: Alexandria
STATE: Virginia
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BARNETT, Richard Spence
MCLACHLAN, Karen Retta
(703) 836-2021
                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                      NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE S
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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LENGTH: 18986 base pairs;
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-819-866-2
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Best Local Similarity 78.2%;
Matches 585; Conservative
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CCCAAATCTTGTGACAAAACTCACACAT 748
                                                                                                              GGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG 540
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                                                         ACCTACATCTGCAACGTGAATCACAAGCCCAGCCAACACCAAGGTGGACAAGAAGTTGAG 720
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Search completed: July 20, 2001, 02:35:29 Job time: 6202 sec

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pir2:PH0958
pir2:S46394
pir2:S29257
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pir2:S34014
pir2:B33548
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pir2:PH0955
pir2:C33548
pir2:S14683
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pir2:S36260
pir2:PH0962
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Pir2:PH0952
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Query: US-08-487-283A-12_COPY_58_423
Query length: 366
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                                                                                                                         pir1:HVHUHG
pir2:PL0086
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Database length: 76174552
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pir2:B32274
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pir2:S20783
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pir2:E30562
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-Q-/cgn2_1/USPTO_spool/US08487283/runat_19072001_075204_168/app_query.fasta_1.444
-DB-pIR_68 -QFMT-fastan -SUFFIX-fra.rpr -GAPOP-12.000
-GAPEXT=4.000 -MINNATCH-0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -MINNATCH-0.100 -LOOPCL=0.000 -XGAPEXT=0.500
-QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pot
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
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-USER-US08487283_@CGN1_1_107 -NCPU-6 -:
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                                                     2:PL0105
2:PH1669
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              seq_documentation_block:
Ig heavy chain V region (clone alpha-MUC1-1) -
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pir2:A30577
pir2:S36271
pir2:S38492
pir2:B22769
pir2:PH1667
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck Blochem. Blophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells A; Reference number: A32483; MUID:89273586
A; Accession: A32483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-487-283A-12_COPY_58_423
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    Quality:
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C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
Ig heavy chain V region - human (fragment)
seq_name: pir2:S36265
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                                                                   GGGTCAAGGAACCCTGGTCACTGTCTCGAGC 366
                                                                                                 LeuAlaThrThrIlePheGlyValLeuIleIleThrGlyMetAspTyrTr
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human (fragment)

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A; Residues: 1-129 <FIG>

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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 *sequence_revision 03-Feb-1994 *text_change 23-Jul-1999
C;Accession: S36255
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448
A;Accession: S36255
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>A;Cross-references: EMBL:Z18846; NID:933121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
C:Accession: $46393
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A; Mitle: In, vitro assembly of repertoires of antibody chains on A:Reference number: $46390; MUID:94254092
A; Accession: $46393
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                           erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTrp
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4.250
91.803
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Gaps:
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                                                                                                                                                                                    20-Jun-2000
                                                                                             surface
                                                                                         of phage
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Ig heavy chain V region (27.7.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Accession: C30562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:231680; NID:g509786; PIDN:CAA83485.1; PID:g1335146 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                              C;Superfamily: immunoglobulin V region; imm C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <II
                                                                                                                                                                            A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen A;Reference number: A30562; MUID:89110066
A;Accession: C30562
A;Status: preliminary
alignment_scores:
                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-119 <SIK>
                                                                                                                                                                                                                                                                       R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, J. Immunol. 142, 888-893, 1989
                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:C30562
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US-08-487-283A-12_COPY_58_423 x S46393
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||LeAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyTr
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4.210
86.822
                                                                   homology <IMM>
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                                                                                                                  immunoglobulin homology
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Gaps:
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72.093
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Percent Similarity:

Quality:

Ratio:

467.50 4.289 89.344

Percent Identity:

70.492

Gaps:

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Ig heavy chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C;Accession: E30562
                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin V region; immun
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b A;Reference number: A30562; MUID:89110066
A;Accession: E30562
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US-08-487-283A-12_COPY_58_423 x C30562
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US-08-487-283A-12_COPY_58_423 x E30562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-119 <SIK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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J. Immunol. 142, 888-893, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:E30562
                                                                                                                                                           Align seg 1/1 to: E30562 from: 1 to: 119
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                                                                                                     CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
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AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGA 100
                                                 GlnValGlnLeuGlnGlnSerGlyAlaGluLeuMetLysProGlyAlaSe
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Ratio:
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4.261
89.344
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Percent Identity:
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A; Molecule type: mRNA
A; Residues: 1-119 <515.
G; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen A;Reference number: A30562; MUID:89110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (27.4b.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-487-283A-12_COPY_58_423 x D30562
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                                                                                                                      301 TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT
                                       151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
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IlePheProGlySerGlySerSerAsnTyrSerGluLysPheLysGlyLy
                                                                                leGluTrpValLysGlnArgProGlyHisGlyLeuGluTrpIleGlyGlu
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4.225
89.344
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Percent Identity:
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autoantibodies.

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Ig heavy chain V-I region (WIL2) - human
() Species: Homo sapiens (man)
() Species: Homo sapiens (man)
() Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
() Accession: D33548
(RKipps, T.J.: Tomhave, E.; Pratt, L.F.: Duffy, S.; Chen, P.P.; Carson, D.A.
(Rrips, T.J.: Tomhave, E.; Pratt, L.F.: Duffy, S.; Chen, P.P.; Carson, D.A.
(Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
(A) Filt: Developmentally restricted immunoglobulin heavy chain variable region gene expt
(A) Reference number: A33548; MUID:89345575
(A) Accession: D33548
(A) Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
(A) Molecule type: mRNA
(A) Residues: 1-123 (RIP)
(C) Keywords: heterotetramer; immunoglobulin
(C) Keywords: heterotetramer; immunoglobulin homology
(C) Keywords: heterotetramer; immunoglobulin homology < NMM>
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US-08-487-283A-12_COPY_58_423 x D33548
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Quality:
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Percent Similarity:
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                                             298 TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAAC 347
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  GGTCACTGTCTCGAGC
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                                                                                      uValThrValSerAla
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                                                                                                                                  sAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeuS
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4.168
89.431
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Percent Identity: 72.358
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|PheAlaTyrTrpGlyGlnGlyThrLe
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A; Residues: 1-135 <MAH>
A; Residues: 1-135 <MAH>
A; Cross-references: EMBL: Z46348; NID: g560839; PIDN: CAA86467.1; PID: g560840
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 34-117/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text
                                                                  seq_documentation_block:
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US-08-487-283A-12_COPY_58_423 x S49530
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A;Accession: S49530
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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                                                                                                           seq_name: pir2:PH0954
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250 86

103

69 150 53

200

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R; Martin,
                                                                       Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text
C;Accession: PH0952
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F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
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A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0954
R; Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880
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Quality:
Ratio:
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F;51-67/Region: complementarity-determining
F;68-98/Region: framework 3
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C; Keywords: heterotetramer;
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A; Residues: 1-132 <MAR>
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                                                                                                                                                                                           seq_name: pir2:PH0952
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;Keywords: heterotetramer; immunoglobulin
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;Martin, T.; Duffy,
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4.183
82.576
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Gaps:
Percent Identity:
                                                                                           17-Apr-1993 #text_change
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69.697
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                                                                                           16-Aug-1996
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F;51-67/Region: complementarity-determining F;68-98/Region: framework 3 F;99-116/Region:
                                                                                  R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors A;Reference number: S23623; MUID:92158804
A;Accession: S23623
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A:Status: preliminary
A:Molecule type: 'DNA
A;Residues: 1-171 <OLE>
A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
                                                                                                                                                                                                                Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
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F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining
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US-08-487-283A-12_COPY_58_423 x PH0952
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A; Residues: 1-128 <M
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A;Status: nucleic acid sequence not shown
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Ratio:
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4.156
85.156
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Percent Identity:
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D.A

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Ig heavy chain V region - human (fragment)
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
(;Accession: S31600
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Reference number: S31585
A;Accession: S31600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-136 <CUI>
A;Reference runce (MRNA)
A;Residues: 1-136 <CUI>
A;Reference runce (MRNA)
A;Residues: 1-136 <CUI>
A;Reference (MRNA)
A;Residues: 1-136 <CUI
                                                                                                                                                                                        A;Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
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US-08-487-283A-12_COPY_58_423 x S23623
                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 CCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCG...CGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 TTTTTGGTTCTAGC......CCGAATTGGTATTTTGATGTTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 gValThrLeuThrArgAspThrSerIleSerThrAlaTyrMetGluLeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 IleAsnProAsnSerGlyGlyThrGlyTyrGlyGlnLysPheGlnGlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 etHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTrp
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                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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4.194
85.714
                              451.00
4.295
   84.677
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Percent Identity:
                              Length:
Gaps:
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   72.581
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R;Mortari, F.; Wang, J.; Schroeder, H.W. submitted to the EMBL Data Library, April 1992 A;Description: Analysis of human cord blood Ig A;Reference number: S20764 A;Accession: S20783 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-487-283A-12_COPY_58_423 x S31600
                                                                                                                    alignment_block:
US-08-487-283A-12_COPY_58_423 x S20783
                                                                                                                                                                                                                            alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z11957; NID:g33899; PIDN:CAA78014.1; PID:g33900 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-121 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S20783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:S20783
                                                                                Align seg 1/1 to: S20783 from: 1
                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain V region - human
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                                           1 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
yThrMetValThrValSerSer 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGGTTCTAGCCCGAATTGG....TATTTTGATGTTTGGGGTCAAGG
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                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                     450.50
4.171
87.097
                                                                                                                                                                                       Percent Identity:
                                                                                  to: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy chain
                                                                                                                                                                                     124
2
73.387
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AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGA 100

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F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-116 <MARP C;Superfamily: immunoglobulin V region; imm C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PHO95
                                                                                                                                                                                                                                                                   alignment_block:
US-08-487-283A-12_COPY_58_423 x PH0959
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F;99-104/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0959
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Ig heavy chain V region
                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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F;68-98/Region: framework 3
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                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: immunoglobulin V region; immunoglobulin homology
345
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                                                                                                                                              {\tt IleAsnProHisGlyGlySerThrThrPheAlaGlnLysLeuGlnGlyAr}
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                                                             rValLysValSerCysLysAlaSerGlyGlyThrPheSerSerTyrAlaI
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                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                   450.00
4.286
86.066
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                                                                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                   122
2
74.590
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C;

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Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-125 <MAR>
C; Superfamily: immunoglobulin V region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies
                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-487-283A-12_COPY_58_423 x PH0957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;68-98/Region: 1
F;99-113/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;31-35/Region: complementarity-determining F;36-50/Region: framework 2 F;55-67/Region: complementarity-determining F;68-98/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: heterotetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: PH0952; MUID:92202880 A; Accession: PH0957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:PH0957
                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-30/Region: framework
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Swissprot 39: HV48_MOUSE +
Swissprot 39: HV1A_HUMAN +
Swissprot 39: HV1A_HUMAN +
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Swissprot 39: HV14_MOUSE +
Swissprot 39: HV04_MOUSE +
Swissprot 39: HV04_MOUSE +
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SwissProt_39:HV1B_HUMAN
SwissProt_39:HV01_MOUSE
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119 | P01810 mus musculus (mouse 114 | P01810 mus musculus (mouse 114 | P01741 mus musculus (mouse 115 | P01807 mus musculus (mouse) 117 | P01749 mus musculus (mouse) 118 | P01809 mus musculus (mouse) 119 | P01759 mus musculus (mouse) 117 | P06326 homo sapiens (human) 136 | P01759 mus musculus (mouse) 117 | P01812 mus musculus (mouse) 117 | P01812 mus musculus (mouse) 117 | P01754 mus musculus (mouse) 118 | P01750 mus musculus (mouse) 119 | P01750 mus musculus (mouse) 119 | P01751 homo sapiens (human) 119 | P01771 homo sapiens (human) 119 | P01788 mus musculus (mouse) 119 | P01789 mus musculus (mouse) 119 | P01791 mus musculus (mouse) 119 | P01791 mus musculus (mouse) 119 | P01791 mus musculus (mouse) 119 | P01793 |
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MEDLINE=81234548;
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from: HV07\_MOUSE

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Gaps: Identity:

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SwissProt_39:HV1D_HUMAN +
SwissProt_39:HV1E_HUMAN +
SwissProt_39:HV14_MOUSE +
SwissProt_39:HV3D_HUMAN +
SwissProt_39:HV3I_HUMAN +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: SwissProt_39:HV07_MOUSE
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    "Heavy chain variable region antibodies: somatic mutation Cell 24:625-637(1981).
-i- MISCELLANEOUS: THE B1-8 MAKING ANTIBODIES TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
                                                                                                                                                                                  InterPro; IPR003006; -. Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                EMBL; J00529; AAA381
PIR; A02034; MHMS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                       (NPB ANTIBODIES).
                                                                                                                                                                                                                                AAA38170.1; -.
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Paskind M., Reth
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                                                                                                                                                                   Signal.
         IG HEAVY CHAIN V REGION B1-8/186
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
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.2e-28
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P01761
P01758
P01765
P01770
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alignment_scores:
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Ratio:
Percent Similarity:
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                                                                                                                                  InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
Homo sapiens (Human).
                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         SEQUENCE
                                                                                                                     CHAIN
                                                                                                                                                                                                           EMBL; J00240; AAA52988.1;
                                                                                                                                                                                                                                                                                                                                                        (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01743;
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                                                                                                                     HEAVY CHAIN V-I REGION HG3.
Gaps:
Identity:
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alignment_block:
US-08-487-283A-12_COPY_58_423 x HV01_MOUSE
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US-08-487-283A-12_COPY_58_423 x HV1B_HUMAN
                                                                                                                alignment_scores:
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Align seg 1/1
                                                                     Percent Similarity:
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region.
NON_TER 121 121
SEQUENCE 121 AA; 13135 M
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MPC 11.
                                                                                                                                                                                                                                           Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
-I- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                            MEDLINE-81053741; PubMed=6253904;
Zakut R., Cohen J., Givol D.;
Zoloning and sequence of the cDNA corresponding
region of immunoglobulin heavy chain MPC11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 to:
HV01_MOUSE
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seq_name: SwissProt_39:HV1C_HUMAN
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CHAIN
MOD_RES
DISULFID
CONFLICT
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21-JUL-1986 (Rel. 01, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
IG HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).
                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                Immediate hypersensitivi
Marcel Dekker, New York
-i- MISCELLANEOUS: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
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                                                                                           SIGNAL
                                                                                                     Pfam; PF00047;
Immunoglobulin
                                                                                                                           PIR; A02026;
                                                                                                                                                                                                Bennich
                                                                                                                                                                                                           SEQUENCE OF 20-147
                                                                                                                                                                                                                              "Cloning and sequence determination of the gene for the rimmunoglobulin epsilon chain expressed in a myeloma cell Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                  Kenten J.H., Molgaard H.V., Bell L.O., Gould H.J.;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-83065234; PubMed-6815656;
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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M.K. (eds.);
hypersensitivity:
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EPSILON CHAIN
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                                                                                                                                                                       modern concepts and developments, pp.1-36,
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          IH -> HI (IN REF. 2)
VG -> GV (IN REF. 2)
MISSING (IN REF. 2)
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                                                                     IG HEAVY CHA
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                                                                   HEAVY CHAIN V-I REGION NE RROLIDONE CARBOXYLIC ACID.
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alignment_scores:
    Quality:
    Ratio:
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US-08-487-283A-12_COPY_58_423 x HV1C_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
HV1G_HUMAN STANDARD;
                                                                                                                                        SEQUENCE FROM N.A.
MEDLIND-88296408; PubMed-2841108;
Matsuda F., Lee K.H., Nakai S., Si
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segmu
                                                                                                                                                                                                                                                                                                 P23083;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328
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                                                                                                            heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .SerAspProPheTrpSerAspTyrTyrAsnPheAspTyrSerTy
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                                                                                                                                                                         Sato T.,
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                                                                                                                                                                           Kodaira M.,
                                                                                                                                                                                                                                                          Hominidae;
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alignment_block:
US-08-487-283A-12_COPY_58_423
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                                                                                                                                                                                                                                                                                                              documentation_block:
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Pfam; PF00047; ig; 1.
Immunoglobulin V region;
1
                                                                   antibodies: somatic mutation Cell 24:625-637(1981).
                                                                                                                     MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                      103
                                                                                                                                                                                                                                                                                                                                                                                                                                       201 TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                                                                          Baltimore D.;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                        P01755;
                                                                                                                                                                                                                                                                                                   HV11_MOUSE
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                                                                                             "Heavy chain variable region
                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION S43 PRECURSOR.
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                                       MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
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                            (NPB ANTIBODIES).
SWISS-PROT entry is copyright.
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seq_documentation_block:
ID HV12_MOUSE STAN
AC P01756;
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                                                                                                                                                                                                                                                                                                                    TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT
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                                                                                                      SwissProt_39:HV12_MOUSE
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JH2 SEGMENT.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
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COMPLEMENTARITY-DETERMINING
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Gaps:
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alignment_block:
US-08-487-283A-12_COPY_58_423
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InterPro; IPR003006; -.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Glycoprotein.
DISULFID 22 96 BY SIMILARITY.
CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
NON_TER 117 117
SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequenc)
15-JUL-1999 (Rel. 38, Last annotat)
IG HEAVY CHAIN V REGION MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy chain constant region domains.";
Biochemistry 21:3415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN
PROTEIN HAS ALSO BEEN DETERMINED.
-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                    ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                                                                                                                                                                                                 {\tt GluValGlnLeuGlnGlnSerGlyProGluLeuValLysProGlyAlaSe}
                                                                                                                                                                                                                                                                                                                                                                                              rValLysMetSerCysLysAlaSerGlyTyrThrPheThrAspTyrTyrM
                                                                                                                                                   snSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgAspTyr 100
                                                                                                                                                                                                                                                                                                                                   etLysTrpValLysGlnSerHisGlyLysSerLeuGluTrpIleGlyAsp
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                                rValThrValSerSer 117
                                                            GGTCACTGTCTCGAGC 366
                                                                                                                      TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT
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   SwissProt_39:HV50_MOUSE
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Ratio:
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3.861
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Last annotation update)
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Gaps:
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alignment_block:
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    Pfam; PF00047; 1g; 1

    Immunoglobulin v region.

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    DOMAIN
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HY50_MOUSE STANDARD; PRT; 120 AA

P06329;

01-JAN-1988 (Rel. 06, Created)

01-JAN-1988 (Rel. 06, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

IG HEAVY CHAIN V REGION AC38 15.3.
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InterPro; IPR003006; -.
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
                                                                                                                                                                                                                                                                                                   151
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GGTCACTGTCTCGAGC 366
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|rValThrValSerSer 120
                                                                                                                                                  TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT::::|||:::|||
                                                                                 TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCT
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                                                              Tyr.....GluGlyAspArgTyrPheAspValTrpGlyThrGlyThrTh
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seq\_name: SwissProt\_39:HV03\_MOUSE

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alignment_block:
US-08-487-283A-12_COPY_58_423
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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PIR; A02028; HVMSG7.

InterPro; IPR003006; -.

Pfam; PF00047; ig; 1.

Immunoglobulin V region; Antiarsonate antibody; Hybridoma.

NON_TER 120 120
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Eur. J. Immunol. 12:1023-1032(1982).
-i- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marshak-Rothstein A.; "The genetic basis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-83131846; PubMed-6186498;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                         {\tt rThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuArgS}
                                                                                                                                                                                              TACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCTCCA 253
                                                                                                                                                                                                                                                          TTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGT
                                                                                                                                                                                                                                                                                        snTrpValLysGlnArgProGlyGlnGlyLeuGluTrpIleGlyTyrIle
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CCTGGTCACTGTCTCGAGC 366
                                                                                                                                                                                                                             AsnProGlyAsnGlyTyrThrLysTyrAsnGluLysPheLysGlyLysTh
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                                                                          TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAAC 347
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Ratio:
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alignment_block:
US-08-487-283A-12_COPY_58_423 x HV13_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: HV13_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                            101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schilling J., Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextrearrangements in heavy chain V-region gene segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATUTE 283:35-40(1980).

-!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION J558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV13_MOUSE
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                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAGCCAGGGGCCTC
GGTCACTGTCTCGAGC 366
                        Tyr.....
                                                           TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGGTCAAGGAACCCT
                                                                                         snSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgAspArg
                                                                                                                        sAlaThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuA
                                                                                                                                                                                  TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                                                                                                                                                                                  IleAsnProAsnAsnGlyGlyThrSerTyrAsnGlnLysPheLysGlyLy
                                                                                                                                                                                                                                               ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                                                                                                                                            rValLysMetSerCysLysAlaSerGlyTyrThrPheThrAspTyrTyrM
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Ratio:
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3.859
84.426
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Gaps:
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alignment_block:
US-08-487-283A-12_COPY_58_423 x HV48_MOUSE
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HYMST7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-UIL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 TGTTACTATGACGCGTGACACTTCGACTAGTACAGGTATACATGGAGCTCT ::::||||:::||| ||| ||| ||||:::|||||||:::|||||
                                                                                            151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tucker P.W.;
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MEDLINE=84248078; PubMed=6429663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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delta in an TdD-secreting plasmacytoma ":
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                                                                                                                                                                                                                               1 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
GlnValGlnLeuGlnGlnProGlyAlaGluLeuValLysProGlyAlaSe
                    sAlaThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuS
                                                                                                                                                                  rValGlnLeuSerCysLysAlaSerGlyHisThrPheThrAsnTyrTrpI
                                                                     IleAsnProAsnAspGlyArgSerAsnTyrAsnGluLysPheLysAsnLy
                                                                                                                   leHisTrpValLysGlnArgProGlyGlnGlyLeuGluTrpIleGlyGlu
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                                                                                                                                                                                                                                                                 to: HV48_MOUSE
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3.886
81.452
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Gaps:
Percent Identity:
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING
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alignment_block:
US-08-487-283A-12_COPY_58_423 x HV02_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Osage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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P01746;
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Pfam; PF00047; ig; 1.
Immunoglobulin V region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
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                                                                                                                                 51 AGTCAAAGTGTCCTGTAAAGCTAGCGGGCTATATTTTTTTCTAATTATTGGA 100
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Ratio:
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obulin heavy chain.";
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3.760
82.927
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-08-487-283A-12_COPY_58_423
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                                                                                                                                                              Align seg 1/1 to: HV51_MOUSE from: 1 to: 118
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SEQUENCE
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION AC38 205.12.
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Pfam; PF00047; ig; 1.
Immunoglobulin V region
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Dildrop.R., Bovens J., Slekevitz M.,
"A V region determinant (idiotope) ex
lymphocytes is encoded by a large set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                            17 rValLysIleSerCysLysAlaSerGlyTyrThrPheThrAspTyrTyrM
                                                            1 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
                                                                                      CCTGGTCACTGTCTCGAGC 366
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idiotope) expressed at high frequency in B
a large set of antibody structural genes.";
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alignment_scores:
Quality:
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ID HV1A_HUMAN STANDARD;
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Align seg 1/1
                                                                Percent Similarity:
                                                                                                                                           DISULFID NON_TER SEQUENCE
                                                                                                                                                                                                                                            "The covalent structure of a human gamma G-immunoglobulin. Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
-i- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
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                                                                                                                                                                                                                                                                                                                                                                "The covalent structure of a human gamma G-immunoglobulin. VII. acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U.,
Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V-I REGION EU.
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MEDLINE=71064027; PubMed=4923144;
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to: HV1A_HUMAN
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Gaps:
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AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTATTGGA 100

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alignment_block:
US-08-487-283A-12_COPY_58_423
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Quality:
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                                                                                                                                    Pfam; PF00047; ig; 1.
Immunoglobulin V region.
NON_TER 119 119
                                                                                                                                                                        PIR; A02078; AVMST6.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; -.
                                                                                                                                                                                                                           complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
                                                                                                                                                                                                                                                                   MEDLINE-79223895; PubMed-111245;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in
immunoglobulin heavy chains from anti-galactan myeloma prote
its potential role in generating diversity in
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION T601.
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P01808;
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                                                         sPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnMetS
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-Q=/cgn2_1/USPTO_spool/US08487283/runat_19072001_075205_227/app_query.fasta_1.444
-DB=SPTREMBL_16 -QFMT=fastan -SUFFIX=tra.rspt -GAPOP=12.000
-GAPEXT=4.000 -MIMMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=-0.000
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-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
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DE MYOSIN-REACTIVE IMMUN
OS HOMO Sapiens (Human).
OC Eukaryota; Metazoa; C
OC Mammalia; Eutheria; P
OX NCBI_TaxID=9806;
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE IPRO03596;
DR InterPro; IPRO03596;
DR InterPro; IPRO03596;
DR InterPro; IPRO03596;
DR InterPro; IPRO03596;
DR Ffam; PF00047; if; 1.
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01-MAY-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGM Homo sapiens (Human).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
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ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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TyrValValProAlaAlaPheSerArgPheAspTyrTrpGlyGlnGl 117
                      TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
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Ratio:
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seq_documentation_block:
ID Q9U195
AC Q9U196
AAR-2000 (TrEMBLrel. 13
DT Q1-MAR-2001 (TrEMBLrel. 13
DT Q1-MAR-2001 (TREMBLrel. 16
DE MYOSIN-REACTIVE IMMUNOGLOB
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chorda
OC Amammalia; Eutherla; Primat
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9
RA WUX., Liu B., Van der Mer
RA YOUNG D.C.;
RT fetus.";
AMEDLINE=9827139; PubMed=9
RA WUX., Liu B., Van der Mer
RA YOUNG D.C.;
RT fetus.";
DMAZIT: TO IMMUNOG
CC -1- SIMILARITY: TO IMMUNOG
CC -1- SIMILARITY: TO IMMUNOG
CC -1- SIMILARITY: TO IMMUNOG
CC DAMAIN.
DR EMBL; AF035019; AAD56255.1
DR InterPro; IPR003006; -.
DR Pfam; PF00047; 1q; 1.
DR SMART; SMO0406; IGV; 1.
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516
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US-08-487-283A-12_COPY_58_423 x Q9UL95
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2010 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                  SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
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                                                                                                                                                                                                                                                                                                         99 ...GlyGlyGlyArgGlyLeuTrpPheAspProTrpGlyGlnGlyThrLe
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gValThrMetThrArgAspThrThrIleSerThrAlaTyrMetGluLeuS
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alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9UL89
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    Q9UL89    PRELIMINARY;
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SEQUENCE
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                    213
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SMART; SM00406; IGV; 1.
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InterPro; IPR003596; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                51 LeuGlyIleAlaAsnTyrAlaGlnLysPheGlnGlyArgValThrIleTh
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                                                             TCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTACTATGAC
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Similarity:
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alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9GYZ2
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                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: Q9GYZ2 from: 1 to: 119
                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Song X.T., Feng Z.Q., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy variable region gene of monoclonal anti-idiotypic antibody Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF282622; AAG01452.1; -.
                                                    201
                                                                                                           151
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora;
Trematoda; Digenea; Strigeidida; Schistosomatoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GYZ2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 CGGAGGACACGGCCGTCTATTATTGCGCGCGCGTTATTTTTTTGGTTCTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma
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                                                                                                                                     34 etAsnTrpValArgGlnAlaProGlyHisGlyLeuGluTrpIleGlyTyr
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                                                                                                                                                                                                                                                 1 CAAGTCCAACTGGTGCAATCCGGCGCGCGAGGTCAAGAAGCCAGGGGCCTC
gValThrMetThrThrAspLysSerPheSerThrAlaTyrMetAspLeuA
                                                    TGTTACTATGACGCGTGACACTTCGACTAGTACAGGATACATGGAGCTCT
                                                                              ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                          rValArgValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrTyrM
                                                                                                                                                                                                                      CCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCTGGTCACTGTCTC
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Percent Identity:
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alignment_scores:
Quality:
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US-08-487-283A-12_COPY_58_423 x Q9Z1C4
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                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: Q9Z1C4 from: 1 to: 118
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Q9Z1C4;
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01-MAY-1999 (TrEMBLrel 10, Last sequence update)
01-MAR-2001 (TrEMBLrel 16, Last annotation update)
01-MAR-2001 (TrEMBLrel 16, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003596; -. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2/G4 constant regions block human leukocyte binding to porcine endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Matis L.M., Evans M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 GGTCACTGTCTCGAGC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                                                               AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTAGTTGGA 100
                                                                                                                                                                                                                                                                                   TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCT 350
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                                                        IleTyrProGlyAspGlyAspThrSerTyrThrGlnLysPheArgGlyLy
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                                                                                                                                                      Ratio:
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118 AA;
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4.147
83.607
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SQ OCCURRENCE OCCURREN

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alignment_block:
US-08-487-283A-12_COPY_58_423 x 095978
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                                                                                                                                                      Align seg 1/1 to:
                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095978;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated v somatic mutations within the untranslated regions of rearranged class switch recombinated Ig genes.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 rLeuThrValSerSer 118
                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jox A., Zander
Bohlen H., Dieł
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; -.
InterPro; IPR003596; -.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-PERIPHERAL BLOOD;
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    -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

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                                                                                                   AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTCTAATTATTGGA
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Diehl V., Wolf J.;
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157 ;
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Percent Identity:
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Last annotation update)
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alignment_block:
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Q9Y298;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GG VH PROTEIN PRECURSOR (FRAGMENT).
IGG VH.
IGG VH.
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SEQUENCE FROM N.A.

MEDLINE-98322155; PubMed-9657749;

Jacquemin M.G., Vander Elst L.P.L.;

Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics" and "Mechanism and kinetics of factor VIII inactivation: study with an "Mechanism and kinetics" and "Mechanism and Mechanism                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
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SIGNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406;
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
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O1-MAY-2000 (TIEMBLrel. 13, Created)
O1-MAY-2000 (TIEMBLrel. 13, Last sequence update)
O1-MAY-2001 (TIEMBLrel. 16, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9JL81
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ID Q9JL81 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF206025; AAF69323.1; -.

InterPro: IPR003065; -.
InterPro: IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SM00406; IG; 1.
SMART; SM00406; IG; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                              LeuAsnGlnLysPheLysAspLysAlaThrLeuThrValAspLysSerSe
                                                            TATACCGAAAATTTTAAAGACCGTGTTACTATGACGCGTGACACTTCGAC
                                                                                              lnGlyLeuGluTrpIleGlyMetIleAspProSerAspSerGluThrArg
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alignment_block:
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SEQUENCE
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"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206029; AAF69327.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                            137 AATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACCGAA 186
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Q9JL83 PRELIMINARY;
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EMBL; AF206023; AAF69321.1; -
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REG
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InterPro; IPR003596; -.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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US-08-487-283A-12_COPY_58_423 x Q9QYF0
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InterPro; IPR003596; -.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
SEQUENCE 298 AA; 31867
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"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtracti
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Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
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Mammalia; Eutheria;
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sPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnMetS
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|etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
|etazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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alignment_block:
US-08-487-283A-12_COPY_58_423 x
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Percent Similarity:
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O9JL75;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-MYOSIN IMMUNOCLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF206031; AAF69329.1; -.
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Scince Escore Len Sinos Jeguata/geneseq/Jenneseqp/AA1995 DAT: AAR77617 + SIDSB/gcgdata/geneseq/geneseqp/AA1995 DAT: AAR77617 + SIDSB/gcgdata/geneseq/geneseqp/AA1995 DAT: AAR77617 + SIDSB/gcgdata/geneseq/geneseqp/AA1995 DAT: AAR77616 + SIDSB/gcgdata/geneseq/geneseqp/AA1995 DAT: AAR77609 + SIDSB/gcgdata/geneseq/geneseqp/AA1995 DAT: AAR77609 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW90935 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW90935 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW90933 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802210 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802210 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802217 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802217 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802217 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802217 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802211 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802212 + SIDSB/gcgdata/geneseq/geneseqp/AA1999 DAT: AAW802216 + SIDSB/gcg
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Database sequences: 412676
Database length: 60623988
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-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM-ext -MINLEN=0 -MAXLEN=20000000
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-USER-EUS08487283_@CGN1_1_85 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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-Q-/cgn2_1/USPTO_spool/US08487283_runat_19072001_075203_141/app_query.fasta_1.444
-DB-A_Geneseq_0601 -QEMT-fastan -SUFFIX-tra.rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPELT=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
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Copyright (c) 1993-2000 Compugen
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seq_documentation_block:
ID AAR77607 standard;
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/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY26984
/SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:AAR24251
/SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:AAR54758
/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:AAY26986
                                                   Humanised CDR-grafted 5G1.1 scFv CB (AAR77607) is the product of a DNA construct (AA708479) derived from DNA of hybridoma ATCC HB 11625, the producer of anti-C5 monoclonal antibody (MAb) 5G1.1. Recombinant scFv CB is obtd. by expression of this DNA in Escherichia coli using vector pET Trc SO5/NI. The light and/or heavy chain CDRs of scFv CB can be combined with CDRs from other 5G1.1-derived antibodies, Fds and light chains (AAR77606-16) in the prodn. of recombinant, including humanised, antibodies that retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular to block human complement C5a generation and thus to reduce glomerular to block human complement C5a generation and thus to reduce glomerular to block human complement C5a generation and thus to reduce glomerular to block human complement C5a generation and thus to reduce glomerular to block human complement C5a generation and thus to reduce glomerular to block human complement C5a generation and thus to reduce glomerular to block human complement C5a generation and thus to reduce glomerular the combined that the combined the combined that the combined the combined that the combined
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                                                                                                                                                                                                                                                            Example 11;
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                                     inflammation and kidney dysfunction associated
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                                                                                                                                                                                                                                                          Page 110-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Springhorn
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Sequence

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XX U2-APR-1996 (first e
XX Humanised 5G1.1 VH +
XX Complement C5; haemol
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    Quality:
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Ratio: 5.344
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody; antiinflammatory; antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised 5G1.1 VH + IGHRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTTCTAATTATTGGA 100
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                                                                                                                                                                                                                                                 1..19
/label= sig_peptide
20..249
/label= mat_peptide
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      94US-0236208
                                                                   95WO-US05688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determining region;
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alignment_block:
US-08-487-283A-12_COPY_58_423 x AAR77611
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Ratio: 5.344
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         framework sequence-altered Fd 5G1.1 VH + IGHRL (AAR77610), which includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned together with DNA (AAT08484) coding for a humanised light chain (AAR77612) into vector APEX-3P (AAT08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
 136
                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang
                                                                                                        103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 38; Page 123-125; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT08484.
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                                                                                                                                                                                     201 TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
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                                                                                                                                                                                                                                                                                                                  CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
                    GGTCACTGTCTCGAGC 366
                                                                                                                                                                                                                                                                            , У,
uValThrValSerSer 141
                                                    PheGlySerSerProAsnTrpTyrPheAspValTrpGlyGlnGlyThrLe
                                                                TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT
                                                                                                                                                         ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
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t  - to inhibit complement induced cell lysis
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, Springhorn
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orn J P,
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Squinto SP,
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100.000
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/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR77615

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alignment_scores:
Quality:
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US-08-487-283A-12_COPY_58_423 x AAR77615
                                                               Align seg 1/1
                                                                                                           Ratio:
Percent Similarity:
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AAR77615 standard;
                                                                                                                                                                                A DNA construct (AAT08487) codes for a humanised CDR-grafted light chain, designated SG1.1 VL + IGHRLD (AAR77615), which incliCDRs derived from mouse anti-C5 monoclonal antibody SG1.1. The DNA can be subcloned together with DNA (AAT08484) coding for a humanised fed (AAR77611) into vector APEX-3P (AAT08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb SG1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR.
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                     Claim 37; Pages 135-137; 181pp; English.
                                                                                                                                                                                                                                                                                                        component
                                                                                                                                                                                                                                                                                                                 Treating
                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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Rother RP, Springhorn
Wang Y, Wilkins JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-1994;
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51 AGTCAAAGTGTCCTGTAAAAGCTAAGCGGCTATATTTTTTCTAATTATTGGA
                            20
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                                    CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
                           GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe
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DB; AAT08487.
                                                                                                                                                                                                                                                                                                      glomerulonephritis with antibody against complement C5
t - to inhibit complement induced cell lysis
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99.180
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Gaps:
Percent Identity:
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iinto SP,
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Thomas TC;
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seq_name:
WPI; 1995-392923/50
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seq_documentation_block:
ID AAR77616 standard; Protein;
Evans MJ, Matis L, Rother RP, Springho Wang Y, Wilkins JA;
                                                                             02-MAY-1994;
                                                                                                    01-MAY-1995;
                                                                                                                              09-NOV-1995.
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                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody; antiinflammatory; antibody
humanised antibody; complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                     Complement C5; haemolysis; kidney; glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised CDR-grafted 5G1.1 scFv DO12.
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                                                   (ALEX-) ALEXION PHARM INC.
                                                                                                                                                       WO9529697-A1
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                                                                                                                                                                                                                                                                                                                                                                                  chain
               Matis L, Mu
Springhorn
                                                                                                                                                                                                                                                                                                                                                                                antibody;
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                                                                             94US-0236208
                                                                                                      95WO-US05688
                                                                                                                                                                                           /label=
225..23
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                                                                                                                                                                                                                     176..186
                                                                                                                                                                                                                                                                                /label= CDR-L2
                                                                                                                                                                                                                                                                                                       /label= CDR-L1
                                                                                                                                                                                                                               'label= CDR-H1
                                                                                                                                                                                                                                                       'label= CDR-L3
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                           Mueller
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                JР,
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               EE, Nye SH,
Squinto SP,
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               Rollins S;
Thomas TC;
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region; CDR;
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alignment_block:
US-08-487-283A-12_COPY_58_423 x AAR77616
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                                                                                                                                                seq_name: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR77610
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                                                                                                                        documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A humanised CDR-grafted scFv, designated 5G1.1 scFv DO12 (AAR77616), includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The scFv can be expressed in Escherichia coli MEI cells by subcloning of encoding DNA (AAT08488) into vector pET Trc SO5/N1. This humanised, recombinant antibody retained the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
Complement @5; haemolysis; kidney; glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT08488
                          Humanised 5G1.1 VH + IGHRL
                                                     15-MAR-1996
                                                                                                           AAR77610 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page 138-140; 181pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                                       GGTCACTGTCTCGAGC
                                                                                                                                                                                                                                               TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT 350
                                                                                                                                                                                                                                                                                                                                                           TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uValThrValSerSer
                                                                                                                                                                                                                                                                                                                                             gValThrMetThrArgAspThrSerThrSerThrValTyrMetGluLeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    leGlnTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGlu
                                                                                                                                                                                                                                  PheGlySerSerProAsnTrpTyrPheAspValTrpGlyGlnGlyThrLe
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Ratio:
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                                                    (first entry)
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5.149
99.180
                                                                                                           Protein;
                                                                                                                                                                                                       366
                                                                                                                                                                              248
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Gaps: 0
Percent Identity: 95.082
                                                                                                           249 AA
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alignment_block:
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                                                                                                                             Align seg 1/1
                                                                                                                                                  US-08-487-283A-12_COPY_58_423 x AAR77610
                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                   A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH + IGHRL (AAR77610), includes CDRs derived from mouse anti-C5 monoclon antibody 5G1.1. It can be co-expressed with a humanised light chain (AAR77612) in human 293 EBNA cells using encoding DNAs subcloned into vector APEX-3P (AAT08476). Such humanised recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang
Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans MJ, Matis L, Rother RP, Springh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR.
                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page 119-122; 181pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-1994;
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                                          36
                                                                                  1995-392923/50.
                                                                                                                                                                                                        Quality:
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Springhorn J P,
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20: 249
/label= mat_peptide
45: 54
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5.142
98.361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR-H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR-H1
                                                                                                                             from: 1
                                                                                                                                                                                    Percent Identity:
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Squinto
                                                                                                                              to: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nye
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94.262
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                                                                                                                                                                                                                                                                                                                                    monoclonal
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seq_name:
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Example 11; Page 107-110; 181pp; English
                          Treating glomerulonephritis with antibody against complement component - to inhibit complement induced cell lysis
                                                                                                                     Evans MJ, Matis L, M
Rother RP, Springhorn
Wang Y, Wilkins JA;
                                                                                                                                                                                  (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                02-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single chain antibody; scFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine 5G1.1M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1996
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                                                                         1995-392923/50.
DB; AAT08479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR77606
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                                                                                                                                                                                                                94US-0236208
                                                                                                                                                                                                                                              95WO-US05688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 28..34
                                                                                                                                                                                                                                                                                                                                       /label= CDR-H3
                                                                                                                                                                                                                                                                                                                                                                                                                  156..159
                                                                                                                                                                                                                                                                                                                                                                     /label= CDR-H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR-L1
                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR-L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR-L2
                                                                                                                                                                                                                                                                                                                                                                                                 .abel- CDR-H1
                                                                                                                                   Mueller
orn J P,
                                                                                                                                                                                                                                                                                                                                                       236
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                                                                                                                                     EE, Nye
Squinto
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                                                                                                                                     Nye SH, nto SP,
                                                                                                                                     Rollins S
Thomas TC;
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Complement C5; haemolysis; kidney; glomerulonephritis; monocional antibody; antiinflammatory; antibody engine humanised antibody; complementarity determining region chimeric antibody; Fab.

ineering; ion; CDR;

Chimeric heavy chain 5G1.1M1 VL 02-APR-1996 (first entry)

HuG1.

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alignment_block:
US-08-487-283A-12_COPY_58_423 x AAR77606
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                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine scFv 5G1.1M1 (AAR77606) is the product of a DNA construct (AAT08479) obtd. from DNA of hybridoma ATCC HB 11625, which produces anti-C5 monoclonal antibody (MAD) 5G1.1. Recombinant scFv 5G1.1M1 is obtd. by expression of this DNA in Escherichia coli using vector pET Trc SO5/NI. The light and/or heavy chain CDRs of scFv 5G1.1M1 can be combined with CDRs from other 5G1.1-derived antibodies, Fds and light chains (AAR77607-16) in the prodn. of recombinant, including humanised, antibodies that retain the ability of MAD 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160
                                                                                                                                                                                                                                                                                                                                                                                                             193
                                                                                                                                                          AAR77609
                                                                                                                                                                                                                                                              351
                                                                                                                                                                                                                                                                                          227
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                                                                                                                                                                                                                                                                                                                                                    210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTAGTTGGA 100
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                                                                                                                                                                                                                                                                                         GGTCACTGTCTCGAGC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leGlnTrpIleLysGlnArgProGlyHisGlyLeuGluTrpIleGlyGlu
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                                                                                                                                                          standard;
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4.826
94.262
                                                                                                                                                          Protein; 249
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Gaps: 0
Percent Identity: 81.148
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                A DNA construct (AAT08481) codes for chimeric light chain 5G1.1M1 VL HuK (AAR77608), which can form the light chain portion of an Fab. The chimeric light chain includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The DNA can be subcloned with DNA (AAT08482) coding for chimeric Fd (AAR77609) into vector APEX-3P (AAT08476) for prodn. of chimeric Fab in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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N-PSDB; AAT08482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-1994;
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                          201
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                       TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                IlcLeuProGlySerGlySerThrGluTyrThrGluAsnPheLysAspLy
                                                                                                                           rValLysMetSerCysLysAlaThrGlyTyrIlePheSerAsnTyrTrpI
                                                                                                                                                                                                   ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
sAlaAlaPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeuS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Page 116-119; 181pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilkins JA;
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С
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Gaps: 0
Percent Identity: 81.148
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                       250
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seq_documentation_block:
ID AAW90936 standard; PP
AC AAW90936;
XX AAW90936;
XX DT 08-AUG-2000 (first e
XX Humanised HFE7A desi
XX Humanised HFE7A desi
XX AW90936; Anti-a
KW Fas; antibody; human;
KW anti-allergic; anti-r
KW dermatological; immur
KW hepatotropic; antiint
KW hepatotropic; human;
KW Hashimoto disease; rit
KW Goodpasture syndrome; s
KW Synthetic.

XX Sep90663-A2.

XX Sep90663
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                                        immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemically systemicall
                                                                                                                                                                                                                                                                                                                                            molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, inti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 188-189; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardermatological; immunosuppressive; thyromimetic; antirheumatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised HFE7A designed heavy chain HHH type protein.
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DB; AAA11655.
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98JP-0276882.
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          arthritis, graft
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Hashimoto

disease,

versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Croh

Crohn's

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alignment_block:
US-08-487-283A-12_COPY_58_423 x AAW90936
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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardian
                                                        Humanised anti-Fas designed heavy chain Heu 3 protein.
                                                                                                   08-AUG-2000
                                                                                                                                                                               AAW90935 standard; Protein; 470
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Gaps: 2
Percent Identity: 80.000
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immunomodulatory; cardiant;
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alignment\_block: US-08-487-283A-12\_COPY\_58\_423 x AAW90935

alignment\_scores:

Quality: Ratio:

503.50 4.496 89.600

Percent Identity: 78.400

Sequence

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Percent Similarity:

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molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas CC ligand system, by binding to Fas on the cell surface, and prevents CC apoptosis in cells with a normal system, by inhibiting binding between CC apoptosis in cells with a normal system, by inhibiting binding between CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, communomodulatory, dermatological, immunosuppressive, thyromimetic, CC inmunomodulatory, dermatological, immunosuppressive, thyromimetic, cantirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerctic, cardiant and hepatropic activity. (I) induce cantiarteriosclerctic, cardiant and hepatropic activity. (I) induce cappitosis by binding to cell surface Fas or inhibit it by competitive cappitosis by binding (I) are used to treat and/or prevent computation of ligand binding. (I) are used to treat and/or prevent computations host disease, Sjorgen's syndrome, pernicious or hypoplastic canemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin cappendent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral confidence) and transplant reference.
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(B, C or b) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 3 which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel humanized anti-ras antibody-like
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30-SEP-1998;
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98JP-0276882
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Align seg

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AAW90935

from: 1

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seq_documentation_block:
ID AAW62209 standard; PT
XX AAW62209;
XC AAW62209;
XX 21-SEP-1998 (first @
XX 22-SEP-1998 (first @
XX 22-SEP-1998 (first @
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       A humanised anti-HM1.24 antibody has been developed which comprises
                                                                                                                                                                                                                           WPI; 1998-286421/25.
N-PSDB; AAV39396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; human; humanised; anti-HM1.24 antibody; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised anti-HM1.24 antibody H chain V region HEF-RVHa-AHM g-gamma-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHUS ) CHUGAI SEIYAKU KK.
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                                                                            Page 106-107; 210pp; Japanese
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ID AAY02555 standard;
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US-08-487-283A-12_COPY_58_423 x AAW62209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAW62209
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                                                                                                                                                                                                                                                                                                                                                                                         TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAACCCT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                 erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgGlyLeu
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Reconstituted human antibody; peptide antigen HM1.24; framework region;

Humanised H chain V region of antiHM1.24 antibody

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alignment_block:
US-08-487-283A-12_COPY_58_423 x AAY02555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  framework regions modified by amino acid substitutions to provide homogeneity with a previously designed framework region (which may arise from a human or non-human source); and complementary determining regions (CDR) derived from a non-human anti-HMI.24 antibody. The reconstituted antibody is useful in the treatment of diseases in which
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                                                                                                                                                                             151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the surface antigen HM1.24 is implicated such as myeloma. The preser sequence is used in the creation of the antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 86-87; 256pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reconstituted human antibody useful in the treatment of myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-277273/23
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                                                                                                                                                                                                                                                                                                               51 AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTAGTTGGA 100
                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                            1 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
                                             specification describes a reconstituted human antibody recognizing peptide antigen HM1.24. This human antibody contains natural human
TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCT
                                                                                            TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                                                                                                                                                                                                                                                                                                                           GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe
                              erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgGlyLeu
                                                                                                                                                                                                                            etGlnTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlySer
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seq_documentation_block:
ID AAW90933 standard; P
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AC AAW90933;
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XX
      seq_name:
                                                                                 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antivital, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, anti-arteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antiarteriosclerotic; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
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30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Page 169-170; 263pp; English.
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98JP-0276882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tamaki I,
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US-08-487-283A-12_COPY_58_423 x AAW90933
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                                                                                                                                                                                                                                                                                                                                    documentation_block:
nephrotropic; antiinfert1111ty; neuroprocective, _____nephrotropic; humanized; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Sjorgen's syndrome; Crohn's disease; sterility; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 1 which is described in the method of the invention.
                                                                                         dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
                                                                                                                                                                                           Humanised anti-Fas designed heavy chain Heu 2 protein
                                                                                                                                                                                                                                    08-AUG-2000
                                                                                                                                                                                                                                                                                                                  AAW90934 standard;
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                                                                                                                                    anti-allergic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ... TATTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCA 341
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                                                                                                                                                     antibody;
                                                                                                                                                                                                                                                                                                                                                                         /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:AAW90934
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                                                                                                                                                                                                                                  (first entry)
                                                                                                                                  anti-arthritic; antiviral; immunomodulatory; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW90933 from: 1 to:
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                                                                                                                                                   human; anti-inflammatory; anti-anemic; antidiabetic;
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89.600
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alignment\_block: US-08-487-283A-12\_COPY\_58\_423 x AAW90934

Align seg

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to:

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1 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAAGGGGCCTC GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe

alignment\_scores:

Quality:

Ratio:

499.50 4.460 89.600

Percent

Identity:

125 2 77.600

Percent Similarity:

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CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas CC ligand system, by binding to Fas on the cell surface, and prevents CC apoptosis in cells with a normal system, by inhibiting binding between CC Fas and its ligand. The products of the invention have anti-inflammatory, canti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, CC immunomodulatory, dermatological, immunosuppressive, thyromimetic, CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, CC immunomodulatory, dermatological, immunosuppressive, thyromimetic, CC anti-arteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive CC inhibition of ligand binding. (I) are used to treat and/or prevent CC diseases associated with the Fas/Fas ligand system, especially systemic CC upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft CC versus host disease, Sjorgen's Syndrome, pernicious or hypoplastic CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively induce it in abnormal cells but selectively induce it in abnormal cells and selectively induce it in abnormal 
                                                                        cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2 ; Page 174-176; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
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N-PSDB; AAA11645.
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30-SEP-1998;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like
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98JP-0276882.
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                                                    as antibody heavy chain construction.
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seq_name:
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complimentarity determining regions (CDR) of mouse origin, leading to a reshaped humanised antibody. The C regions are human Ck (L-chain) and human C gamma (especially C gamma 1) (H-chain). The FR regions of the
                                   A humanised anti-HM1.24 antibody has been developed which comprises human L and H chain C regions, and L and/or H chain V regions containing material originating in mouse anti-HM1.24 antibody. The V regions contain framework (FR) regions of human origin and
                                                                                                                                                                                                  Koishihara Y,
                                                                                                                                                                                                                                                     04-OCT-1996;
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                                                                                                   Example
                                                                                                                          Humanised anti-HM1.24 antibody -
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                                                                                                                                                                                                                                                                                                                                                                                                             human; humanised; anti-HM1.24 antibody; myeloma; FR;
                                                                                                  9; Page 108-109; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-HM1.24 antibody H chain V region
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                                                                                                                                                                                                   Kosaka
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                                                                                                                                                                                                                                                                          97WO-JP03553.
                                                                                                                                                                                                                                                                                                                                                                                                complimentarity determining region; antigenicity.
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                                                                                                                          myeloma
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alignment_block:
US-08-487-283A-12_COPY_58_423
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                                                                                                                                                                            Reconstituted human antibody; peptide antigen HM1. complementary determining region; CDR; anti-HM1.24
                                                                                                                                                                                                                                                                                                      Humanised H chain V region of antiHM1.24 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY02556 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 GGTCACTGTCTCGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:::||||||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
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Synthetic

humanised antibody.

antibody;

myeloma;

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alignment_block:
US-08-487-283A-12_COPY_58_423 x AAY02556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a reconstituted human antibody recognizing the peptide antigen HM1.24. This human antibody contains natural human framework regions modified by amino acid substitutions to provide homogeneity with a previously designed framework region (which may arise from a human or non-human source); and complementary determining regions (CDR) derived from a non-human anti-HM1.24 antibody. The reconstituted antibody is useful in the treatment of diseases in which the surface antigen HM1.24 is implicated such as myeloma. The present sequence is used in the creation of the antibodies of the invention.
                                                        120
                                                                                  301
                                                                                                                103
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N-PSDB; AAX36291.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reconstituted human antibody useful in the treatment of myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1998;
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sValThrMetThrAlaAspThrSerThrSerThrValTyrMetGluLeuS 103
                                                                                                                                                                                                                          AGTCAAAGTGTCCTGTAAAGCTAGCGGGCTATATTTTTTCTAATTAGTTGGA 100
                          GGTCACTGTCTCGAGC 366
                                                      .....ArgArgGlyGlyTyrTyrPheAspTyrTrpGlyGlnGlyThrTh 134
                                                                       TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCT 350
                                                                                                                                                                                                                                                                                                                                           rValLysValSerCysLysAlaSerGlyTyrThrPheThrProTyrTrpM 53
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Ratio:
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Percent Identity: 78.689
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OM of: U%-08-487-283A-12\_COPY\_58\_423 to: Issued\_Patents\_AA:\*

out\_format :

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Cgn2_6/ptcdata/2/iaa/5E_COMB.pep:US-08-476-7768-18 + 488.50 1046.31 4.9e (Cgn2_6/ptcdata/2/iaa/5E_COMB.pep:US-08-127-721A-18 + 488.50 1046.31 4.9e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-127-721A-18 + 488.50 1046.31 4.9e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-485-246A-18 + 488.50 1046.31 4.9e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-09-199-149-12 + 478.00 1012.63 2.6e 4.0e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-09-199-149-12 + 478.00 1012.92 3.6e 4.0e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-09-199-149-12 + 473.00 1012.92 3.6e 4.0e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-09-199-149-12 + 473.00 1012.92 3.6e 4.0e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-476-176B-12 + 472.50 1012.92 3.6e 4.0e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-127-721A-12 + 472.50 1011.61 4.2e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-127-721A-12 + 472.50 1011.61 4.2e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-127-721A-16 + 471.50 1009.44 5.6e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-476-176B-16 + 471.50 1009.44 5.6e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-447-040-105 + 470.50 1009.32 6.9e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-447-040-105 + 470.50 1009.32 6.9e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-447-040-105 + 470.50 1009.32 6.9e (Cgn2_6/ptcdata/2/iaa/5A_COMB.pep:US-08-4487-201-105 + 470.50 1009.32 6.9e (Cgn2_6/ptcdata/2/iaa/5B_COMB.pep:US-08-4487-201-105 + 470.50 1009.32 6.9e (Cgn2_6/ptcdata/2/iaa/5B_COMB.pep:US-08-4487-105 + 466.50 997.94 2.8e (Cgn2_6/ptcdat
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Query: US-08-487-283A-12_COPY_58_423
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Database length: 20144635
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-LOOPEXT-0.000 -GAPOP-4.500 -GGAPOXT-0.050 -XGAPOP-10.000
-XGAPEXT-0.500 -FGAPOP-6.000 -GGAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -START-1
-MATRIX-blosum62 -TRANS-human40.cdi -LIST-45 -DOCALIGN-200
-THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN-15 -MODE-LOCALI-
-OUTEMI-pfs -NORM-ext -MINLEN-0 -MAXLEN-200000000
-USER-US08487283_@CGN1_1_28 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPX
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-O=/cgn2_1/USPTO_spool/US08487283/runat_19072001_075204_154/app_query.fasta_1.444
-DB-Issued_Patents_AA -OFMT-fastan -SUFFIX-tra.rai
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/ptodata/2/1aa/6A_COMB.pep:US-08-127-7
/ptodata/2/1aa/6A_COMB.pep:US-08-127-7
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3.6e-4
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                              3e-48
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alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-476-176B-14
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/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:PCT-US93:11612-12 + 462.50 990.94
/cgn2_6/ptodata/2/1aa/SB_COMB.pep:PCT-US95-01219-45 + 462.50 990
/cgn2_6/ptodata/2/1aa/SB_COMB.pep:PCT-US95-01219-45 + 462.50 990
/cgn2_6/ptodata/2/1aa/SB_COMB.pep:US-08-253-877C-19 + 462.00 989.06
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-452-164A-19 + 462.00 989.06
                                                                                                                                             Align seg 1/1 to: US-08-476-176B-14 from: 1 to:
                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (908) 277-43
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CITY: East Hanover
CITY: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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51 AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTAGTTGGA 100
                                                            20 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe
                                                                               1 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                           Quality:
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Percent Identity: 77.236
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36 rValLysValSerCysLysAlaSerGlyTyrThrPheSerMetTyrTrpL

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AFFLACE.

FILING DATE: 27-SEPTEMBER: 21-SEPTEMBER: 22-SEPTEMBER: 24-SEPTEMBER: 25-SEPTEMBER: 37-952,802

FILING DATE: 25-SEPTEMBER-1992

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6066718ak, Henry P.

RECISTRATION NUMBER: 33,200

REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP

TELECOMMUNICATION INFORMATION:

"TTIEPHONE: (908) 277-5110
                       alignment_scores:
                                                                                US-08-127-721A-14
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Patent No. 6066718
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                                                                                                                                                                                                        NFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPA+11
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,721A
FILING DATE: 27-SEPTEMBER-1993
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                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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CITY: E
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ZIP: 07936-1080
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STATE: New Jersey
                                                                                                                                                                  LENGTH:
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Quality:
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Saldanha, Jose
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    493.50
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    Length:
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alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-127-721A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
                                                                                                                                                         COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                    FILING DATE:
                                                                                                                                      APPLICATION NUMBER: US/08/485,246A
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Saldanha, Jose
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seq_documentation_block:
; Sequence 78, Application US/08428257A
; Patent No. 5885808
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US-08-487-283A-12_COPY_58_423 x US-08-485-246A-14
                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/laa/5B_COMB.pep:US-08-428-257A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: NO. 6072035ak, Henry P.
REGISTRATION NUMBER: 3,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELECHONE: (908) 277-5110
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
                                                                                  APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.
TITLE OF INVENTION: Compounds to
NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                  120 HisPheSerGlySerAsnTyrAspTyrPheAspTyrTrpGlyGlnGlyTh 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAGCCAGGGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                     CCTGGTCACTGTCTCGAGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT 250
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                                                                                                                                                                                                                                                                                                                    rLeuValThrValSerSer 142
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGGTTCTAGCCCGAATTGG...TATTTTGATGTTTGGGGTCAAGGAAC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rValLysValSerCysLysAlaSerGlyTyrThrPheSerMetTyrTrpL 53
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New York
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4.446
90.244
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Percent Identity: 77.236
                                                                                                      target cells
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alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-428-257A-78
                                                                                                             seq_documentation_block:
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                                                                                                                                          seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-07-987-264-60
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Percent Similarity:
                                                 Sequence 60, Application US/07987264
Patent No. 6204366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICANT: VERHOEYEN, MARTINE ELISA TITLE OF INVENTION: SPECIFIC BINDIN NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                      101 AspPheAla......TrpPheAlaTyrTrpGlyGlnGlyTh
                                                                                                                                                                                                                                                                                                                                                             151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
                                                                                                                                                                                                                                                                                                                            34 leGluTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                    CCTGGTCACTGTCTCGAGC 366
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                                                                                                                                                                                                                                                                                         TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAAC
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4.441
90.244
   SPECIFIC BINDING 62
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

CUSHMAN, DARBY & CUSHMAN

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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB PCT/GB91/01511
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG 200
                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 9019553.8
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
298 TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAAC 347
                                                                                                                                                      201 TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                 51
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                                                                                                                                                                                                                                                                                                                                                 17 rValLysValSerCysLysAlaSerGlyTyrThrPheSerAlaTyrTrpI 34
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/987,264 FILING DATE: 08-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                        CCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGCGCGCGGT...TAT 297
                                    erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgSerTyr 100
                                                                                                                 gValThrValThrArgAspThrSerThrAsnThrAlaTyrMetGluLeuS 84
                                                                                                                                                                                               IleLeuProGlySerAsnAsnSerArgTyrAsnGluLysPheLysGlyAr 67
                                                                                                                                                                                                                                                                          leGluTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValGlyGlu
                                                                                                                                                                                                                                                                                                                                                                            AGTCAAAGTGTCCTGTAAAGCTAGCGGGCTATATTTTTTCTAATTGGA 100
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20005-3918
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Percent Identity: 78.862
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alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-476-176B-18
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                                                                                                                                                             Align seg 1/1 to: US-08-476-176B-18 from: 1 to: 142
                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08476176B Patent No. 5958708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908) 277-43
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hardman, No. APPLICANT: Kolbinger, E APPLICANT: Saldanha, JC TITLE OF INVENTION: ResTITLE OF INVENTION: imm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILLING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708AK; Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (908) 277-5110
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                  51 AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTCTAATTAGTTGGA 100
                                                                           STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
                                                                                                                     1 CAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 59 Route 1
CITY: East Hanover
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
rValLysValSerCysLysAlaSerGlyTyrThrPheSerMetTyrTrpL 53
                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                   Ratio:
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                                                                                                                                                                                                                                                              Percent Identity: 78.049
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seq_documentation_block:
    alignment_scores:
                                                              US-08-127-721A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08127721A Patent No. 6066718
                                                                                                                                                                                                                CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/952,80
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6066718ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
                                                                                                                                                                              TELEFAX: (908) 277-43
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 rLeuValThrValSerSer 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 HisPheSerGlySerAsnTyrAspTyrPheAspTyrTrpGlyGlnGlyTh 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 59 Route 1
CITY: East Hanover
                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                      LENGTH:
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                                                                                                  amino acid
GY: linear
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                                                                                                                                        142 amino acids
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Saldanha, Jose
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                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-485-246A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILLING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,246A
FILING DATE:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          STREET: 59 RUC-
CITY: East Hanover
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348 CCTGGTCACTGTCTCGAGC 366
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                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                          07936-1080
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Saldanha, Jose
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4.477
89.431
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103 250

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25-SEPTEMBER-1992

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seq_documentation_block:
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US-08-487-283A-12_COPY_58_423 x US-08-485-246A-18
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-246A-18
                                                                                                                                                                                                                                             seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                   Sequence 28, Application US/0794642: Patent No. 5558864
                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (908) 277-4306 INFORMATION FOR SEQ ID NO:
               TITLE OF INVENTION: Humanized a TITLE OF INVENTION: Antibodies NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                  APPLICANT: Bendig, Mary M.
APPLICANT: Kettleborough, Catherine A.
APPLICANT: Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
                                                                                                                                                                                                                                                                                 103
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   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                            TTTGGTTCTAGCCCGAATTGG...TATTTTGATGTTTTGGGGTCAAGGAAC 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt IleSerProGlyThrPheThrThrAsnTyrAsnGluLysPheLysAlaAr}
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                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-946-421-28
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Ratio:
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Millen, White, Zelano & Branigan, P.C.
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4.477
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                                                                         Humanized and Chimeric Monoclonal
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alignment_block:
US-08-487-283A-12_COPY_58_423 x US-07-946-421-28
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-07-946-421-28 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 64191
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04 MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
LENGTH: 140 amino acio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/946,421
FILING DATE: 06-NOV-1992
                                                                                                                                                                           201
                                                                                                                                                                                                                                                                               TELEPHONE: 703-243-6333
120 TyrAspTyrAspGlyArg...TyrPheAspTyrTrpGlyGlnGlyThrLe 135
                                                                                                                                                                                                                                                151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG 200
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REFERENCE/DOCKET NUMBER: Merck 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
                TTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTTGGGGTCAAGGAACCCT 350
                                                                 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe
                                                                                                     {\tt gValThrMetThrLeuAspThrSerThrAsnThrAlaTyrMetGluLeuS}
                                                                                                                                                                         TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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4.350
90.164
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351

GGTCACTGTCTCGAGC 366

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seq_documentation_block
                              seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-199-149-5
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US-08-487-283A-12_COPY_58_423 x US-09-199-149-12
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US-09-199-149-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
FILE REFERENCE: P50860
CURRENT APPLICATION NUMBER: US/09/199,149
CURRENT FILING DATE: 1998-11-24
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6160099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09199149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 128
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                            106 ValArgGlySer......
                                                                                                                                                                                                                           251 CCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC...GCGCGTTAT 297
                                                                                                                                                                                                                                                                                                 201
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                                                                                                                                                             TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAAC 347
                                                                                                                                                                                           rValLysValSerCysLysAlaSerGlyTyrThrPheSerSerTyrTrpI 39
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4.385
88.618
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Percent Identity: 77.236
                                                                                                                                .MetAspTyrTrpGlyGlnGlyTh 117
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 118
TYPE: PRT
ORGANISM: Humanized B9
US-09-199-149-5
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Quality:
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US-08-487-283A-12_COPY_58_423 x US-09-199-149-5
                                 seq_documentation_block:
                                                               seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-202-047-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-199-149-5 from: 1 to: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Sequence 9, Application US/08202047 Patent No. 5800815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09199149 Patent No. 6160099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
FILE REFERENCE: p5080
CURRENT APPLICATION NUMBER: US/09/199,149
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 37
                                                                                                                                        348
                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT
                                                                                                                                                                                                        298 TTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGGTCAAGGAAC 347
                                                                                                                                                                                                                                                                          251 CCAGCCTGCGATCGGAGGACACGGCCGTCTATTATTGC...GCGCGTTAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                     151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                     478.00
4.385
88.618
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Gaps:
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GENERAL INFORMATION:
APPLICANT: CHESNUT
APPLICANT: POLLEY,
APPLICANT: PAULSON

APPLICANT:

CHESNUT, Robert W.
POLLEY, Margaret J.
PAULSON, James C.
JONES, S. Tarran
SALDANHA, Jose W.

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alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-202-047-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-202-047-9 from: 1 to: 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-326-240
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                       151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BENDIG, Mary M.
FITLE OF INVENTION: Antibo
                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                 53 etHisTrpValArgGlnAlaProGlyGlnArgLeuGluTrpMetGlyPhe 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Bolon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/202,047 FILING DATE: 25-FEB-1994 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                     TTTGGTTCTAGCCCG.....AATTGGTATTTTGATGTTTTGGGGGTCAAGG 344
                                                                              erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArg.....
                                                                                                                                                              gValThrIleThrSerAspThrSerAlaSerThrAlaTyrMetGluLeuS
                                                                                                                                                                                                      TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT 250
                                                                                                                                                                                                                                                 IleAsnProSerAsnAspGlyProLysTyrAsnGluArgPheLysAsnAr 86
                                                                                                                                                                                                                                                                                                                                                                                                             rValLysValSerCysLysAlaSerGlyTyrThrPheThrAsnTyrValM 53
.....AlaArgProGlyPheAspTrpTyrPheAspValTrpGlyGlnGl 132
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: California
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4.339
87.903
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alignment_block:
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                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/202,047
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SALDANHA, Jose W.
APPLICANT: BENDIG, Mary M.
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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                   51 AGTCAAAGTGTCCTGTAAAGCTAGCGGCTATATTTTTTTCTAATTATTGGA 100
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/964,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                        /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-964-690-9
                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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amino acid
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415-326-2422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JONES, S. Tarran
SALDANHA, Jose W.
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4.339
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                                                                                                                                                                                                                                                                                                         Percent Identity: 75.806
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alignment_block:
US-08-487-283A-12_COPY_58_423 x US-09-199-149-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3
LENGTH: 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Applic Patent No. 6160099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
FILE REFERENCE: P50860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/199,149
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ATCTTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TTTGGTTCTAGCCCG.....AATTGGTATTTTGATGTTTTGGGGTCAAGG 344
201 TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
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                                                                                                                                                                                             86 gValThrIleThrSerAspThrSerAlaSerThrAlaTyrMetGluLeuS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 rValLysValSerCysLysAlaSerGlyTyrThrPheThrSerTyrAlaI 34
                                                                                                                                                                                                                                                                              53 etHisTrpValArgGlnAlaProGlyGlnArgLeuGluTrpMetGlyPhe 69
                                                                                                                                                                                                                                                                                                                                                                      1 CAAGTCCAACTGGTGCAATCCGGCGCCCGAGGTCAAGAAGCCAGGGGCCTC
                                                                                                                                                                                                                                                                                                                        IleAsnProGly...GlyAspThrAsnTyrAlaGlnLysPheGlnGlyAr 66
                                                                                                                                                   TGTTACTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCT 250
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4.375
85.714
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; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-476-176B-12
                                   alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-476-176B-12
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Align seg 1/1 to: US-08-476-176B-12 from: 1 to: 142
                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Apprint No. 5958708
                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:

NAME: NO. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ. ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 59 NOTES OF STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 yGlnGlyThrLeuValThrValSerSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 TCAAGGAACCCTGGTCACTGTCTCGAGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 TyrGlyTyrGlyGlyGlyCysTyrGlyTyrTrpTyrTrpGlyValTrpGl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 .....TATTTTTTGGTTCTAGCCCGAATTGGTATTTTGATGTTTGGGG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 gValThrIleThrAlaAspThrSerThrSerThrAlaTyrMetGluLeuS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,6
FILING DATE: 25-SEPTEMBER-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/476,176B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07936-1080
                                                                                                                                           Quality:
                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08476176B
                                                                                                                                                                                                                                                                                                            142 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: No. 5958708artis Patent Department 59 Route 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolbinger, Frank
Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hardman, No. 5958708man
                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEPTEMBER-1993
JMBER: US 07/952,802
                                                                                                   476.50
4.372
88.618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reshaped monoclonal antibodies against an
                                                                                                   Percent Identity: 73.984
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     $0.46 Estimated total session cost 0.169 DialUnits
SYSTEM:OS - DIALOG OneSearch
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         (c) 2000 BIOSIS
      73:EMBASE 1974-2000/Oct W3
         (c) 2000 Elsevier Science B.V.
*File 73: Update codes are currently undergoing readjustment.
For details type Help News73.
  File 155:MEDLINE(R) 1966-2000/Dec W4
         (c) format only 2000 Dialog Corporation
*File 155: For changes to the file and check tags information
please see Help News155.
  File 399:CA SEARCH(R) 1967-2000/UD=13320
         (c) 2000 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
RANK charge added; see HELP RATES 399.
  File 357: Derwent Biotechnology Abs 1982-2000/Nov B2
         (c) 2000 Derwent Publ Ltd
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? s 5gl? and (c5 or c5a or complement)
              89 5G1?
           19902 C5
            8617 C5A
          237256 COMPLEMENT
              6 5G1? AND (C5 OR C5A OR COMPLEMENT)
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             2 RD S1 (unique items)
? t s2/3/al1
           (Item 1 from file: 5)
 2/3/1
DIALOG(R) File 5: Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.
           BIOSIS NO.: 199799595493
10974348
Inhibition of complement activity by humanized anti-C5 antibody
  and single-chain Fv.
AUTHOR: Thomas Thomas C(a); Rollins Scott A; Rother Russell P; Giannoni
  Michelle A; Hartman Sandra L; Elliott Eileen A; Nye Steven H; Matis Louis
  A; Squinto Stephen P; Evans Mark J
AUTHOR ADDRESS: (a) Alexion Pharmaceuticals, 25 Science Park, New Haven, CT
  06511**USA
```

```
RECORD TYPE: Abstract
LANGUAGE: English
          (Item 1 from file: 357)
2/3/2
DIALOG(R) File 357: Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.
0190050 DBA Accession No.: 96-00821
                                        PATENT
Treating glomerulonephritis with antibody against complement-C5
    component - antiinflammatory monoclonal antibody production from
    hybridoma cell culture, and Fv single chain antibody engineering
AUTHOR: Evans M J; Matis L; Mueller E E; Nye S H; Rollins S; Rother R
    P; Springhorn J P; Squinto S P; Thomas T C; Wang Y; Wilkins J A
CORPORATE SOURCE: New Haven, CT, USA.
PATENT ASSIGNEE: Alexion-Pharm. 1995
PATENT NUMBER: WO 9529697 PATENT DATE: 951109 WPI ACCESSION NO.:
    95-392923 (9550)
PRIORITY APPLIC. NO.: US 236208 APPLIC. DATE: 940502
NATIONAL APPLIC. NO.: WO 95US5688 APPLIC. DATE: 950501
LANGUAGE: English
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S2
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            8617 C5A
          237256 COMPLEMENT
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? s antibod?(10n) c5 (10n) c5a
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           19902 C5
            8617 C5A
             106 ANTIBOD? (10N) C5 (10N) C5A
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...examined 50 records (100)
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      S5
? t s5/7/all
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JOURNAL: Molecular Immunology 33 (17-18):p1389-1401 1996 (1997)

ISSN: 0161-5890

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s (c5)(20n)(c5a)(20n)(antibod?)
>>>Operator "(5C)" in invalid position
? s (antibod?)(20n)(c5)(20n)(c5a)
>>>Operator "(5C)" in invalid position
? ds
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Set
S1
            6
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S2
            2
               RD S1 (unique items)
? s antibod?(10n)(c5 or c5a or complement)
         1604233 ANTIBOD?
           19902 C5
            8617 C5A
          237256 COMPLEMENT
         52782 ANTIBOD? (10N) (C5 OR C5A OR COMPLEMENT)
? s antibod?(10n) c5 (10n) c5a
         1604233 ANTIBOD?
           19902 C5
            8617 C5A
            106 ANTIBOD?(10N) C5 (10N) C5A
      S4
? rd s4
...examined 50 records (50)
...examined 50 records (100)
...completed examining records
              52 RD S4 (unique items)
      S5
? t s5/7/all
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File 73:EMBASE 1974-2000/Oct W3
         (c) 2000 Elsevier Science B.V.
      73: Update codes are currently undergoing readjustment.
For details type Help News73.
 File 155:MEDLINE(R) 1966-2000/Dec W4
         (c) format only 2000 Dialog Corporation
*File 155: For changes to the file and check tags information
please see Help News155.
  File 399:CA SEARCH(R) 1967-2000/UD=13320
         (c) 2000 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
RANK charge added; see HELP RATES 399.
  File 357: Derwent Biotechnology Abs 1982-2000/Nov B2
         (c) 2000 Derwent Publ Ltd
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>>>'IALOG' not recognized as set or accession number
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           $0.20 0.024 DialUnits File73
     $0.20 Estimated cost File73
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     $0.08 Estimated cost File155
           $0.30     0.024 DialUnits File399
     $0.30 Estimated cost File399
           $0.28 0.024 DialUnits File357
     $0.28 Estimated cost File357
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     $1.04 Estimated cost this search
                                        0.119 DialUnits
     $1.04 Estimated total session cost
File 410:Chronolog(R) 1981-2000 Sep/Oct
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HILIGHT set on as ''
? begin 5,73,155,399,357
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            $0.00 0.059 DialUnits File410
     $0.00 Estimated cost File410
     $0.02 TYMNET
     $0.02 Estimated cost this search
     $1.06 Estimated total session cost 0.178 DialUnits
SYSTEM:OS - DIALOG OneSearch
  File 5:Biosis Previews(R) 1969-2000/Nov W2
         (c) 2000 BIOSIS
  File 73:EMBASE 1974-2000/Oct W3
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(c) 2000 Elsevier Science B.V.
*File 73: Update codes are currently undergoing readjustment.
For details type Help News73.
  File 155:MEDLINE(R) 1966-2000/Dec W4
         (c) format only 2000 Dialog Corporation
*File 155: For changes to the file and check tags information
please see Help News155.
                        1967-2000/UD=13320
  File 399:CA SEARCH(R)
         (c) 2000 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
RANK charge added; see HELP RATES 399.
  File 357: Derwent Biotechnology Abs 1982-2000/Nov B2
         (c) 2000 Derwent Publ Ltd
      Set Items Description
? s c5 (10n) (alpha(w)chain) (10n) antibod?
         19902 C5
1597067 ALPHA
          867947 CHAIN
         1604233 ANTIBOD?
               4 C5 (10N) (ALPHA(W)CHAIN) (10N) ANTIBOD?
      S1
? rd s1
...completed examining records
               2 RD S1 (unique items)
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? t s/7/all
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           (Item 1 from file: 5)
 2/7/1
DIALOG(R) File 5: Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.
           BIOSIS NO.: 000094108458
FORMATION AND STRUCTURE OF THE C5B-7 COMPLEX OF THE LYTIC PATHWAY OF
  COMPLEMENT
AUTHOR: DISCIPIO R G
AUTHOR ADDRESS: DEP. IMMUNOLOGY IMM18, RESEARCH INSTITUTE SCRIPPS CLINIC,
  10666 N. TORREY PINES RD., LA JOLLA, CALIF. 92037.
JOURNAL: J BIOL CHEM 267 (24). 1992. 17087-17094.
FULL JOURNAL NAME: Journal of Biological Chemistry
CODEN: JBCHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH
```

ABSTRACT: The formation and structure of the complement cytolytic intermediary complex, C5b-7, were studied with the aim of determining the interactive regions of C5, C6, and C7. The structure of human complement component C5 was elucidated by the application of limited proteolysis which generated well characterized major polypeptide fragments of this molecule. Plasmin, thrombin, and kallikrein cleave C5b with greater facility than C5. The most useful cleavage of C5b was effected by plasmin because the fragmentation pattern was similar to the processing the C3b by factors H, I, and kallikrein. Plasmin hydrolyzes peptide bonds within the .alpha.'-chain of C5b, resulting in a four-chain fragment, C5c (Mr = 142,000), and a single chain fragment, C5d (Mr = 43,000). Circular dichroism spectroscopic analyses indicated that C5d is substantially richer in .alpha.-helical content than is C5c (27 versus 9%). Polyclonal antibodies directed against C5c blocked the interaction of C5b-6 with C7, whereas antibodies directed against C5d inhibited the binding of C5 with C3b. Chemical cross-linking using a cleavable radioiodinated photoreactive reagent revealed that both C6 and C7

associate preferentially with the .alpha.'-chain of C5b. The reversible interactions of C5 with C6, C7, and major polypeptide fragments derived from these were investigated with solid phase binding assays. The results indicate that the carboxyl-terminal domains of C6 and C7, which have cysteine-rich modules homologous to those found in factors H and I, have the capacity to link specifically with C5.

(Item 1 from file: 357) DIALOG(R) File 357: Derwent Biotechnology Abs (c) 2000 Derwent Publ Ltd. All rts. reserv. 0190050 DBA Accession No.: 96-00821 PATENT Treating glomerulonephritis with antibody against complement-C5 component - antiinflammatory monoclonal antibody production from hybridoma cell culture, and Fv single chain antibody engineering AUTHOR: Evans M J; Matis L; Mueller E E; Nye S H; Rollins S; Rother R P; Springhorn J P; Squinto S P; Thomas T C; Wang Y; Wilkins J A CORPORATE SOURCE: New Haven, CT, USA. PATENT ASSIGNEE: Alexion-Pharm. 1995 PATENT NUMBER: WO 9529697 PATENT DATE: 951109 WPI ACCESSION NO.: 95-392923 (9550) PRIORITY APPLIC. NO.: US 236208 APPLIC. DATE: 940502 NATIONAL APPLIC. NO.: WO 95US5688 APPLIC. DATE: 950501 LANGUAGE: English ABSTRACT: A new method for therapy of glomerulonephritis involves introduction of an antibody (Ab) that binds to complement-C5 into the bloodstream, to reduce the cell-lysing ability of complement present in the blood. The Ab reduces conversion of complement-C5 to complement-C5a and -C5b. The Ab may bind to C5b, and does not inhibit formation of complement-C3b. The Ab may inhibit binding of C5 to complement-C3 or complement-C4, by binding with a 5G46k, 5G27k, 5G325aa, 5G200aa or KSSKC peptide fragment. A complete blockade of complement hemolytic activity may occur. A monoclonal Ab (MAb) against human complement-C5 alpha-chain or a peptide fragment, produced by hybridoma 5G1.1 (ATCC HB 11625) is new. DNA encoding an Fv single chain antibody with specified variable region light chain and heavy
chain sequences (including complementarity determining region-1, -2 and -3) and an optional human constant domain is claimed, and may be inserted in a vector for expression in a recombinant host cell. The MAb eliminates glomerular inflammation and enlargement, and may also be used in therapy of inflammatory joint disease or immunological or blood disorders. (181pp) ? begin 652,653,654 10nov00 09:57:51 User208760 Session D1713.6 \$1.12 0.199 DialUnits File5 \$1.65 1 Type(s) in Format 7 \$1.65 1 Types \$2.77 Estimated cost File5 0.207 DialUnits File73 \$1.76 \$1.76 Estimated cost File73 0.205 DialUnits File155 \$0.66 \$0.66 Estimated cost File155 \$2.75 Estimated cost File399 \$0.63 0.053 DialUnits File357 \$2.20 1 Type(s) in Format 7 \$2.20 1 Types Estimated cost File357 OneSearch, 5 files, 0.883 DialUnits FileOS \$0.15 TYMNET \$10.92 Estimated cost this search \$11.98 Estimated total session cost 1.061 DialUnits

File 652:US Patents Fulltext 1971-1979

(c) format only 2000 The Dialog Corp.

\*File 652: Reassignment data current through 7/25/2000 recordings. Due to recent processing problems, the SORT command is not working. File 653:US Patents Fulltext 1980-1989

(c) format only 2000 The Dialog Corp.

\*File 653: Reassignment data current through 7/25/2000 recordings. Due to recent processing problems, the SORT command is not working. File 654:US Pat.Full. 1990-2000/Nov 07

(c) format only 2000 The Dialog Corp.

\*File 654: Reassignment data current through 7/25/2000 recordings. Due to recent processing problems, the SORT command is not working.

Set Items Description

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19913 C5

310045 ALPHA

351863 CHAIN

45267 ANTIBOD?

S1 0 C5 (10N) (ALPHA(W)CHAIN) (10N) ANTIBOD?

5/7/52 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
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0117029 DBA Accession No.: 91-04671 PATENT

Sensitive assay of complement-C5a peptide or des-Arg derivative - new monoclonal antibody, anti-idiotype monoclonal antibody and hybridoma PATENT ASSIGNEE: Goetze O 1991

PATENT NUMBER: EP 411306 PATENT DATE: 910206 WPI ACCESSION NO.: 91-038259 (9106)

PRIORITY APPLIC. NO.: DE 3924924 APPLIC. DATE: 890727 NATIONAL APPLIC. NO.: EP 90111920 APPLIC. DATE: 900622 LANGUAGE: German

ABSTRACT: A method for the detection and/or quantitative determination of the complement peptides C5a and/or C5a-des-Arg (C5a') in biological fluid comprises immobilized antibodies (Ab 1) which bind C5a and C5a', and second detectable antibodies (Ab 2) which bind to C5a and/or C5a' bound to the first antibodies. The following are claimed: (1) cell lines producing monoclonal antibodies (MAbs) which bind to the receptor-binding sites in C5a and C5a' but not with the corresponding amino acid sequence in native C5; (2) MAbs produced by these cell lines; (3) anti-idiotype (AIAb) against MAb produced by the specified cell lines; and (4) the cell line CNCM I-188 which produces AIAb F23/14. Ab 1 and Ab 2 are MAbs produced in mice or humans, and are MAb C17/5 (produced by the cell line CNCM I-887) and MAb G25/2 (produced by the cell line CNCM I-889), respectively. Compositions containing the MAbs can be used to treat and prevent diseases associated with elevated C5a levels in the blood or other disorders related to intra- or extra-vascular complement activation. AIAb can be used to block reaction of C5a with its receptors. (27pp)

03412845 EMBASE No: 1987165422

Rapid and simple measurement of human C5a-des-Arg level in plasma or serum using monoclonal antibodies

Takeda J.; Kinoshita T.; Takata Y.; et al.

Department of Bacteriology, Osaka University Medical School, Suita, Osaka 565 Japan

Journal of Immunological Methods ( J. IMMUNOL. METHODS ) (Netherlands) 1987, 101/2 (265-270)

CODEN: JIMMB

DOCUMENT TYPE: Journal

LANGUAGE: ENGLISH

A new sandwich immunoassay method for measuring human C5a-des-Arg was developed using monoclonal antibody specifically reactive with C5a-des-Arg. Monoclonal antibodies were obtained from a panel of hybridomas produced by fusion of mouse myeloma cells, P3 x 63-AG8,653, with spleen cells from a CBF1(C57BL/6 x BALB/c) mouse immunized with purified C5a. The reactivities of these monoclonal antibodies against C5a, C5a-des-Arg and C5 were tested by solid-phase radioimmunoassay. One of the antibodies reacted with C5a-des-Arg, but not with C5a and C5. By use of this antibody for capturing antibody in sandwich immunoassay, a rapid and simple method was developed for measuring C5a-des-Arg without previous removal of C5. The sensitivity of this assay system was approximately 1 ng/ml

5/7/35 (Item 4 from file: 73)

DIALOG(R)File 73:EMBASE

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07290420 EMBASE No: 1998173819

Immunotherapy for autoimmune and inflammatory renal diseases Jayne D.R.W.

D.R.W. Jayne, Division of Renal Medicine, St George's Hospital Medical

School, London SW17 ORE United Kingdom

AUTHOR EMAIL: djayne@sghms.ac.uk

Current Opinion in Nephrology and Hypertension ( CURR. OPIN. NEPHROL.

HYPERTENS. ) (United Kingdom) 1998, 7/3 (311-315)

CODEN: CNHYE ISSN: 1062-4821 DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 46

New treatments for autoimmune renal disease are required, and a developing knowledge of its underlying immunopathogenesis has identified sites where immunotherapy is likely to be effective. Experience with intravenous immunoglobulin and lymphocyte depletion by monoclonal antibodies in systemic vasculitis and systemic lupus erythematosus is awaiting confirmation by randomized trials. Treatments at or near clinical testing include monoclonal antibody blockade of leucocyte-endothelial interactions and CD40 mediated B-cell activation, and immunoablation with autologous stem- cell transplantation for more severe multisystem autoimmune disease.

06268778 BIOSIS NO.: 000086102961

DETECTION OF NATIVE HUMAN COMPLEMENT COMPONENTS C3 AND C5 AND THEIR PRIMARY ACTIVATION PEPTIDES C3A AND C5A ANAPHYLATOXIC PEPTIDES BY ELISA WITH MONOCLONAL ANTIBODIES

AUTHOR: KLOS A; IHRIG V; MESSNER M; GRABBE J; BITTER-SUERMANN D AUTHOR ADDRESS: INST. MED. MICROBIOLOGY, HOCHHAUS AM AUGUSTUSPLATZ, 6500 MAINZ, WEST GERMANY.

JOURNAL: J IMMUNOL METHODS 111 (2). 1988. 241-252. FULL JOURNAL NAME: Journal of Immunological Methods

CODEN: JIMMB

RECORD TYPE: Abstract LANGUAGE: ENGLISH

ABSTRACT: Monoclonal antibodies (mAbs) were raised against human C3a, C3b, C5a, and C5b after immunization of BALB/c mice with the native components C3 and C5. Using different combinations of these mAbs we have developed four sensitive sandwich-enzyme-linked immunosorbent assays (ELISAs) for the detection of native C3 or C5 in samples with low concentrations of these proteins, e.g., in cell culture supernatants or synovial fluids and cerebrospinal fluids (CSF) and for the detection of the anaphylatoxic peptides (AT-peptides) C3a or C5a in human EDTA-plasma. The C3- and C5-ELIS as were found to be specific for the uncleaved complement proteins. Two different anti-C3a or anti-C5a mAbs were combined for the C3a- and C5a-eLISA. Before assaying a sample in the C3a- or C5a-ELISA a precipitation step to eliminate uncleaved C3 and C5 was necessary. The sensitivity and specificity of the four ELISAs were treated with purified antigens and EDTA-plasma or Cobra venom factor-activated EGTA-plasma samples as a source of C3a and C5a. The detection limits were 1 ng/ml for C3, 1 ng/ml for C3a, 2 ng/ml for C5, and 100 pg/ml for C5a. Plasma samples from patients undergoing cardiopulmonary bypass (CPB) surgery were used as a source of pathological material.

10225205 BIOSIS NO.: 199698680123

In vitro and in vivo inhibition of complement activity by a single-chain Fv fragment recognizing human C5.

AUTHOR: Evans Mark J(a); Rollins Scott A; Wolff Dennis W; Rother Russell P; Norin Allen J; Therrien Denise M; Grijalva Galo A; Mueller John P; Nye Steven H; Squinto Stephen P; Wilkins James A

AUTHOR ADDRESS: (a) Dep. Molecular Dev., Alexion Pharmaceuticals, 25 Science Park, New Haven, CT 06511\*\*USA

JOURNAL: Molecular Immunology 32 (16):p1183-1195 1995

ISSN: 0161-5890

DOCUMENT TYPE: Article RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: Complement activation has been implicated in the pathogenesis of several human diseases. Recently, a monoclonal antibody (N19-8) that recognizes the human complement protein C5 has been shown to effectively block the cleavage of C5 into C5a and C5b, thereby blocking terminal complement activation. In this study, a recombinant N19-8 scFv antibody fragment was constructed from the N19-8 variable regions, and produced in both mammalian and bacterial cells. The N19-8 scFv bound human C5 and was as potent as the N19-8 monoclonal antibody at inhibiting human C5b-9-mediated hemolysis of chicken erythrocytes. In contrast, the N19-8 scFv only partially retained the ability of the N19-8 monoclonal antibody to inhibit C5a generation. To investigate the ability of the N19-8 scFv to inhibit complement-mediated tissue damage, complement-dependent myocardial injury was induced in isolated mouse hearts by perfusion with Krebs-Henseleit buffer containing 6% human plasma. The perfused hearts sustained extensive deposition of human C3 and C5b-9, resulting in increased coronary artery perfusion pressure, end-diastolic pressure, and a decrease in heart rate until the hearts ceased beating approximately 10 min after the addition of plasma. Hearts treated with human plasma supplemented with either the N19-8 monoclonal antibody or the N19-8 scFv did not show any detectable changes in cardiac performance for at least 1 hr following the addition of plasma. Hearts treated with human plasma alone showed extensive deposition of C3 and C5b-9, while hearts treated with human plasma containing the N19-8 scFv showed extensive deposition of C3, but no detectable deposition of C5b-9. Administration of a 100 mg bolus dose of N19-8 scFv to rhesus monkeys inhibited the serum hemolytic activity by at least 50% for up to 2 hr. Pharmacokinetic analysis of N19-8 scFv serum levels suggested a two-compartment model with a T-1/2-alpha of 27 min. Together, these data suggest the recombinant N19-8 scFv is a potent inhibitor of the terminal complement cascade and may have potential in vivo applications where short duration inhibition of terminal complement activity is desirable.

5/7/13 (Item 13 from file: 5)
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10061787 BIOSIS NO.: 199598516705

Anti-C5 monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease.

AUTHOR: Wang Yi(a); Rollins Scott A(a); Madri Joseph A; Matis Louis A(a) AUTHOR ADDRESS: (a) Immunobiol. Program, Alexion Pharm. Inc., New Haven, CT 06511\*\*USA

JOURNAL: Proceedings of the National Academy of Sciences of the United

States of America 92 (19):p8955-8959 1995

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DOCUMENT TYPE: Article RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: Activated components of the complement system are potent mediators of inflammation that may play an important role in numerous disease states. For example, they have been implicated in the pathogenesis of inflammatory joint diseases including rheumatoid arthritis (RA). To target complement activation in immune-mediated joint inflammation, we have utilized monoclonal antibodies (mAbs) that inhibit the complement cascade at C5, blocking the generation of the major chemotactic and proinflammatory factors C5a and C5b-9. In this study, we demonstrate the efficacy of a mAb specific for murine C5 in the treatment of collagen-induced arthritis, an animal model for RA. We show that systemic administration of the anti-C5 mAb effectively inhibits terminal complement activation in vivo and prevents the onset of arthritis in immunized animals. Most important, anti-C5 mAb treatment is also highly effective in ameliorating established disease. These results demonstrate a critical role for activated terminal complement components not only in the induction but also in the progression of collagen-induced arthritis and suggest that C5 may be an attractive therapeutic target in RA.

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5/7/9 (Item 9 from file: 5)
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10514607 BIOSIS NO.: 199699135752

Amelioration of lupus-like autoimmune disease in NZB/W F-1 mice after treatment with a blocking monoclonal antibody specific for complement component C5.

AUTHOR: Wang Yi(a); Hu Qile; Madri Joseph A; Rollins Scott A; Chodera Amy; Matis Louis A

AUTHOR ADDRESS: (a) Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT 06511\*\*USA

JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 93 (16):p8563-8568 1996

ISSN: 0027-8424

DOCUMENT TYPE: Article RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: New Zealand black times New Zealand white (NZB/W) F-1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F-1 mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 months of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic complement activation, the role of proinflammatory complement components in disease progression has not been established. In this study we have examined the contribution of activated terminal complement proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F-1 mice were treated with a monoclonal antibody (mAb) specific for the C5 component of complement that blocks the cleavage of C5 and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for 6 months resulted in significant amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal complement cascade in the progression of renal disease in NZB//W F-1 mice, and suggest that mAb-mediated C5 inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.

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DIALOG(R)File 5:Biosis Previews(R)
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10419584 BIOSIS NO.: 199699040729

Proteolytic inactivation of the leukocyte C5a receptor by proteinases derived from Porphyromonas gingivalis.

AUTHOR: Jagels Mark A(a); Travis James; Potempa Jan; Pike Robert; Hugli Tony E

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(Item 4 from file: 5) 5/7/4 5:Biosis Previews(R) DIALOG(R)File (c) 2000 BIOSIS. All rts. reserv.

BIOSIS NO.: 199800298553 11517221

Myocardial infarction and apoptosis after myocardial ischemia and reperfusion: Role of the terminal complement components and inhibition by anti-C5 therapy.

AUTHOR: Vakeva Antti P; Agah Azin; Rollins Scott A; Matis Louis A; Li Lan; Stahl Gregory L(a)

AUTHOR ADDRESS: (a) Cent. Exp. Ther. and Reperfusion Injury, Dep. Anesth.,

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JOURNAL: Circulation 97 (22):p2259-2267 June 9, 1998

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ABSTRACT: Background-Myocardial ischemia and reperfusion (MI/R)-induced tissue injury involves necrosis and apoptosis. However, the precise contribution of apoptosis to cell death, as well as the mechanism of apoptosis induction, has not been delineated. In this study, we sought to define the contribution of the activated terminal complement components to apoptosis and necrosis in a rat model of MI/R injury. Methods and Results-Monoclonal antibodies (mAbs; 18A and 16C) raised against the rat C5 complement component bound to purified rat C5 (ELISA). 18A effectively blocked C5b-9-mediated cell lysis and C5a -induced chemotaxis of rat polymorphonuclear leukocytes (PMNs), whereas 16C had no complement inhibitor activity. A single dose (20 mg/kg IV) of 18A blocked >80% of serum hemolytic activity for >4 hours. Administration of 18A before myocardial ischemia (30 minutes) and reperfusion (4 hours) significantly reduced (91%) left ventricular free wall PMN infiltration compared with 16C treatment. Treatment with 18A 1 hour before ischemia or 5 minutes before reperfusion significantly reduced infarct size compared with 16C treatment. A significant reduction in infarct size (42%) was also observed in 18A-treated rats after 30 minutes of ischemia and 7 days of reperfusion. DNA ladders and DNA labeling (eg, TUNEL assay) demonstrated a dramatic reduction in MI/R-induced apoptosis in 18A-treated compared with 16C-treated rats. Conclusions-Anti-C5 therapy in the setting of MI/R significantly inhibits cell apoptosis, necrosis, and PMN infiltration in the rat despite C3 deposition. We conclude that the terminal complement components C5a and C5b-9 are key mediators of tissue injury in MI/R.

5/7/6 (Item 6 from file: 5)
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11340383 BIOSIS NO.: 199800121715

Controlling the complement system in inflammation.

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JOURNAL: Immunopharmacology 38 (1-2):p51-62 Dec., 1997

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DOCUMENT TYPE: Literature Review

RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: Inappropriate or excessive activation of the complement system can lead to harmful, potentially life-threatening consequences due to severe inflammatory tissue destruction. These consequences are clinically manifested in various disorders, including septic shock, multiple organ failure and hyperacute graft rejection. Genetic complement deficiencies or complement depletion have been proven to be beneficial in reducing tissue injury in a number of animal models of severe complement-dependent inflammation. It is therefore believed that therapeutic inhibition of complement is likely to arrest the process of certain diseases. Attempts to efficiently inhibit complement include the application of endogenous soluble complement inhibitors (C1-inhibitor, recombinant soluble complement receptor 1-rsCR1), the administration of antibodies, either blocking key proteins of the cascade reaction (e.g. C3, C5), neutralizing the action of the complement-derived anaphylatoxin C5a , or interfering with complement receptor 3 (CR3, CD  $\overline{18/11b}$ )-mediated adhesion of inflammatory cells to the vascular endothelium. In addition, incorporation of membrane-bound complement regulators (DAF-CD55, MCP-CD46, CD59) has become possible by transfection of the correspondent cDNA into xenogeneic cells. Thereby, protection against complement-mediated inflammatory tissue damage could be achieved in various animal models of sepsis, myocardial as well as intestinal ischemia/reperfusion injury, adult respiratory distress syndrome, nephritis and graft rejection. Supported by results from first clinical trials, complement inhibition appears to be a suitable therapeutic approach to control inflammation. Current strategies to specifically inhibit complement in inflammation have been discussed at a recent meeting on the 'Immune Consequences of Trauma, Shock and Sepsis', held from March 4-8, 1997, in Munich, Germany. The Congress (chairman: E. Faist, Munich, Germany), which was held in close cooperation with various national and international shock and trauma societies, was attended by about 2000 delegates from 40 countries. The major objective of the meeting was to provide an overview on the most state-of-the-art methods to prevent multiple organ dysfunction syndrome (MODS)/multiple organ failure (MOF) following the systemic inflammatory response (SIRS) to severe trauma. One of the largest symposia held within the Congress was devoted to current aspects of controlling complement in inflammation (for abstracts see: Shock 1997, 7 Suppl., 71-75). After providing the audience with information on the scientific background by addressing the clinical relevance of complement activation (G.O. Till, Ann Arbor, MI, USA) and discussing recent developments in modern complement diagnosis (J. Kohl, Hannover, Germany), B.P. Morgan (Cardiff, UK) introduced the symposium's special issue by giving an overview on complement regulatory molecules. Selected topics included overviews on the application of C1 inhibitor (C.E. Hack, Amsterdam, NL), sCRI (U.S. Ryan, Needham, MA, USA),

antibodies to C5 (Y. Wang, New Haven CT, USA) and to the anaphylatoxin C5a (M. Oppermann, Gottingen, Germany), and a report on complement inhibition in cardiopulmonary bypass (T.E. Mollnes, Bodo, Norway). The growing interest of clinicians in complement-directed anti-inflammatory therapy, and the fact that only some of the various aspects of therapeutic complement inhibition could be addressed on the meeting, has motivated the author to expand a Congress report into a short comprehensive review on recent strategies to control complement in inflammation.

5/7/7 (Item 7 from file: 5)
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10974348 BIOSIS NO.: 199799595493

Inhibition of complement activity by humanized anti-C5 antibody and single-chain Fv.

AUTHOR: Thomas Thomas C(a); Rollins Scott A; Rother Russell P; Giannoni Michelle A; Hartman Sandra L; Elliott Eileen A; Nye Steven H; Matis Louis A; Squinto Stephen P; Evans Mark J

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JOURNAL: Molecular Immunology 33 (17-18):p1389-1401 1996 (1997)

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RECORD TYPE: Abstract LANGUAGE: English

ABSTRACT: Activation of the complement system contributes significantly to the pathogenesis of numerous acute and chronic diseases. Recently, a monoclonal antibody (5G1.1) that recognizes the human complement protein C5, has been shown to effectively block C5 cleavage, thereby preventing the generation of the pro-inflammatory complement components C5a and C5b-9. Humanized 5G1.1 antibody, Fab and scFv molecules have been produced by grafting the complementarity determining regions of 5G1.1 on to human framework regions. Competitive ELISA analysis indicated that no framework changes were required in the humanized variable regions for retention of high affinity binding to C5, even at framework positions predicted by computer modeling to influence CDR canonical structure. The humanized Fab and scFv molecules blocked complement-mediated lysis of chicken erythrocytes and porcine aortic endothelial cells in a dose-dependent fashion, with complete complement inhibition occurring at a three-fold molar excess, relative to the human C5 concentration. In contrast to a previously characterized anti-C5 scFv molecule, the humanized h5G1.1 scFv also effectively blocked C5a generation. Finally, an intact humanized h5G1.1 antibody blocked human complement lytic activity at concentrations identical to the original murine monoclonal antibody. These results demonstrate that humanized h5G1.1 and its recombinant derivatives retain both the affinity and blocking functions of the murine 5G1.1 antibody, and suggest that these molecules may serve as potent inhibitors of complement-mediated pathology in human inflammatory diseases.

5/7/8 (Item 8 from file: 5)
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10825740 BIOSIS NO.: 199799446885

Monoclonal antibody to C5 inhibits C5a and C5b-9

generation without inhibition of C3 cleavage and significantly limits myocardial ischemia and reperfusion induced tissue damage.

AUTHOR: Vakeva A(a); Rollins S A; Matis L A; Stahl G L

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JOURNAL: Journal of the American College of Cardiology 29 (2 SUPPL. A):p 267A 1997

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10514607 BIOSIS NO.: 199699135752

Amelioration of lupus-like autoimmune disease in NZB/W F-1 mice after treatment with a blocking monoclonal antibody specific for complement component C5.

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JOURNAL: Proceedings of the National Academy of Sciences of the United

States of America 93 (16):p8563-8568 1996

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ABSTRACT: New Zealand black times New Zealand white (NZB/W) F-1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F-1 mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 months of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic complement activation, the role of proinflammatory complement components in disease progression has not been established. In this study we have examined the contribution of activated terminal complement proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F-1 mice were treated with a monoclonal antibody (mAb) specific for the C5 component of complement that blocks the cleavage of C5 and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for 6 months resulted in significant amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal complement cascade in the progression of renal disease in NZB//W F-1 mice, and suggest that mAb-mediated C5 inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.